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(57) Abstract

Nucleic acid sequences encoding ϵ–cyclase, isopentenyl pyrophosphate isomerase and β–carotene hydroxylase as well as vectors containing the same and hosts transformed with the vectors. Methods for controlling the ratio of various carotenoids in a host and for the production of novel carotenoid pigments. The present invention also provides a method for screening for eukaryotic genes encoding carotenoid biosynthesis, and for modifying the disclosed enzymes.

GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND METHODS OF USE THEREOF

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention describes nucleic acid sequences for eukaryotic genes encoding ε lycopene ε-cyclase (also known as ε-cyclase and ε lycopene cyclase), isopentenyl pyrophosphate isomerase (IPP) and β-carotene hydroxylase as well as vectors containing the same and hosts transformed with said vectors. The present invention also provides methods for augmenting the accumulation of carotenoids, changing the composition of the carotenoids, and producing novel and rare carotenoids. The present invention provides methods for controlling the ratio or relative amounts of various carotenoids in a host. The invention also relates to modified lycopene ε-cyclase, IPP isomerase and β-carotene hydroxylase. Additionally, the present invention provides a method for screening for genes and cDNAs encoding enzymes of carotenoid biosynthesis and metabolism.

Background of the Invention

Carotenoid pigments with cyclic endgroups are essential components of the photosynthetic apparatus in oxygenic photosynthetic organisms (*e.g.*, cyanobacteria, algae and plants; Goodwin, 1980). The symmetrical bicyclic yellow carotenoid pigment β-carotene (or, in rare cases, the asymmetrical bicyclic α-carotene) is intimately associated with the photosynthetic reaction centers and plays a vital role in protecting against potentially lethal photooxidative damage (Koyama, 1991). β-carotene and other carotenoids derived from it or from α-carotene also serve as light-harvesting pigments (Siefermann-Harms, 1987), are involved in the thermal dissipation of excess light energy captured by the light-harvesting antenna (Demmig-Adams & Adams, 1992), provide substrate for the biosynthesis of the plant growth regulator abscisic acid (Rock & Zeevaart, 1991; Parry & Horgan, 1991), and are precursors of vitamin A in human and animal diets (Krinsky, 1987). Plants also exploit carotenoids as coloring agents in flowers and fruits to attract pollinators and agents of seed dispersal (Goodwin, 1980). The color provided by carotenoids is also of agronomic value in a number of important crops. Carotenoids are currently harvested from a variety of organisms, including plants, algae, yeasts, cyanobacteria and bacteria, for use as pigments in food and feed.

The probable pathway for formation of cyclic carotenoids in plants, algae and cyanobacteria is illustrated in Figure 1. Two types of cyclic endgroups or rings are commonly found in higher plant carotenoids, these are referred to as the β (*beta*) and ϵ (*epsilon*) rings (Fig. 3). The precursor acyclic endgroup (no ring structure) is referred to as the Ψ (*psi*) endgroup. The β and ε endgroups differ only in the position of the double bond in the ring. Carotenoids with two β rings are ubiquitous, and those with one β and one ϵ ring are common, but carotenoids with two ϵ rings are uncommon. β-carotene (Fig. 1) has two β-endgroups and is a symmetrical compound that is the precursor of a number of other important plant carotenoids such as zeaxanthin and violaxanthin (Fig. 2).

Genes encoding enzymes of carotenoid biosynthesis have previously been isolated from a variety of sources including bacteria (Armstrong et al., 1989, Mol. Gen. Genet. 216, 254-268; Misawa et al., 1990, J. Bacteriol., 172, 6704-12), fungi (Schmidhauser et al., 1990, Mol. Cell. Biol. 10, 5064-70), cyanobacteria (Chamovitz et al., 1990, Z. Naturforsch, 45c, 482-86; Cunningham et al., 1994) and higher plants (Bartley et al., Proc. Natl. Acad. Sci USA 88, 6532-36; Martinez-Ferez & Vioque, 1992, Plant Mol. Biol. 18, 981-83). Many of the isolated enzymes show a great diversity in structure, function and inhibitory properties between sources. For example, phytoene desaturases from the cyanobacterium *Synechococcus* and from higher plants and green algae carry out a two-step desaturation to yield ζ-carotene as a reaction product. In plants and cyanobacteria a second enzyme (ζ-carotene desaturase), similar in amino acid sequence to the phytoene desaturase, catalyzes two additional desaturations to yield lycopene. In contrast, a single desaturase enzyme from *Erwinia herbicola* and from other bacteria introduces all four double bonds required to form lycopene. The *Erwinia* and other bacterial desaturases bear little amino acid sequence similarity to the plant and cyanobacterial desaturase enzymes, and are thought to be of unrelated ancestry. Therefore, even with a gene in hand from one source, it may be difficult to identify a gene encoding an enzyme of similar function in another organism. In particular, the sequence similarity between certain of the prokaryotic and eukaryotic genes encoding enzymes of carotenoid biosynthesis is quite low.

Further, the mechanism of gene expression in prokaryotes and eukaryotes appears to differ sufficiently such that one cannot expect that an isolated eukaryotic gene will be properly expressed in a prokaryotic host.

The difficulties in isolating genes encoding enzymes with similar functions is exemplified by recent efforts to isolate the gene encoding the enzyme that catalyzes the formation of β-carotene from the acyclic precursor lycopene. Although a gene encoding an enzyme with this function had been isolated from a bacterium, it had not been isolated from any photosynthetic procaryote or from any eukaryotic organism. The isolation and characterization of the enzyme catalyzing formation of β-carotene in the cyanobacterium *Synechococcus* PCC7942 was described by the present inventors and others (Cunningham et al., 1993 and 1994). The amino acid sequence similarity of the cyanobacterial enzyme to the various bacterial lycopene β–cyclases is so low (*ca.* 18-25% overall; Cunningham et al., 1994) that there is much uncertainty as to whether they share a common ancestry or, instead, represent an example of convergent evolution.

The need remains for the isolation of eukaryotic and prokaryotic genes and cDNAs encoding polypeptides involved in the carotenoid biosynthetic pathway, including those encoding a lycopene ϵ-cyclase, IPP isomerase and β-carotene hydroxylase. There remains a need for methods to enhance the production of carotenoids, to alter the composition of carotenoids, and to reduce or eliminate carotenoid production. There also remains a need in the art for methods for screening for genes and cDNAs encoding enzymes of carotenoid biosynthesis and metabolism.

SUMMARY OF THE INVENTION

Accordingly, a first object of this invention is to provide purified and/or isolated nucleic acids which encode enzymes involved in carotenoid biosynthesis; in particular, lycopene ϵ-cyclase , IPP isomerase and β-carotene hydroxylase.

A second object of this invention is to provide purified and/or isolated nucleic acids which encode enzymes which produce novel or uncommon carotenoids.

A third object of the present invention is to provide vectors containing said genes.

A fourth object of the present invention is to provide hosts transformed with said vectors.

Another object of the present invention is to provide hosts which accumulate novel or uncommon carotenoids or which accumulate greater amounts of specific or total carotenoids.

Another object of the present invention is to provide hosts with inhibited and/or altered carotenoid production.

Another object of this invention is to secure the expression of eukaryotic carotenoid-related genes in a recombinant prokaryotic host.

Yet another object of the present invention is to provide a method for screening for eukaryotic and prokaryotic genes and cDNAs which encode enzymes involved in carotenoid biosynthesis and metabolism.

An additional object of the invention is to provide a method for manipulating carotenoid biosynthesis in photosynthetic organisms by inhibiting the synthesis of certain enzymatic products to cause accumulation of precursor compounds.

Another object of the invention is to provide modified lycopene ε-cyclase, IPP isomerase and β-carotene hydroxylase.

These and other objects of the present invention have been realized by the present inventors as described below.

A subject of the present invention is an isolated and/or purified nucleic acid sequence which encodes for a protein having lycopene ε-cyclase, IPP isomerase or β-carotene hydroxylase enzyme activity and having the amino acid sequence of SEQ ID NOS: 2, 4, 14-21 or 23-27.

The invention also includes vectors which comprise any of the nucleic acid sequences listed above, and host cells transformed with such vectors.

Another subject of the present invention is a method of producing or enhancing the production of a carotenoid in a host cell, comprising inserting into the host cell a vector comprising a heterologous nucleic acid sequence which encodes for a protein having lycopene ε-cyclase, IPP isomerase or β-carotene hydroxylase enzyme activity, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence to produce the protein.

Yet another subject of the present invention is a method of modifying the production of carotenoids in a host cell, the method comprising inserting into the host cell a vector comprising a heterologous nucleic acid sequence which produces an RNA and/or encodes for a protein which modifies lycopene ε-cyclase, IPP isomerase or β-carotene hydroxylase enzyme activity, relative to an untransformed host cell, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence in the host cell to modify the production of the carotenoids in the host cell, relative to the untransformed host cell.

The present invention also includes a method of expressing, in a host cell, a heterologous nucleic acid sequence which encodes for a protein having lycopene ε-cyclase, IPP isomerase or β-carotene hydroxylase enzyme activity, the method comprising inserting into the host cell a vector comprising the heterologous nucleic acid sequence, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence.

Also included is a method of expressing, in a host cell, a heterologous nucleic acid sequence which encodes for a protein which modifies lycopene ε-cyclase, IPP isomerase or β-carotene hydroxylase enzyme activity in the host cell, relative to an untransformed host cell, the method comprising inserting into the host cell a vector comprising the heterologous nucleic acid sequence, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence.

Another subject of the present invention is a method for screening for genes and cDNAs which encode enzymes involved in carotenoid biosynthesis and metabolism.

BRIEF DESCRIPTION OF THE DRAWINGS

A more complete appreciation of the invention and many of the attendant advantages thereof will be readily obtained as the same becomes better understood by reference to the following detailed description when considered in connection with the accompanying drawings, wherein:

Figure 1 is a schematic representation of the putative pathway of β-carotene biosynthesis in cyanobacteria, algae and plants. The enzymes catalyzing various steps are indicated at the left. Target sites of the bleaching herbicides NFZ and MPTA are also indicated at the left. Abbreviations: DMAPP, dimethylallyl pyrophosphate; FPP, farnesyl pyrophosphate; GGPP, geranylgeranyl pyrophosphate; GPP, geranyl pyrophosphate; IPP, isopentenyl pyrophosphate; LCY, lycopene cyclase; MVA, mevalonic acid; MPTA, 2-(4-methylphenoxy)triethylamine hydrochloride; NFZ, norflurazon; PDS, phytoene desaturase; PSY, phytoene synthase; ZDS, ζ-carotene desaturase; PPPP, prephytoene pyrophosphate.

Figure 2 depicts possible routes of synthesis of cyclic carotenoids and common plant and algal xanthophylls (oxycarotenolds) from neurosporene. Demonstrated activities of the β- and ε-cyclase enzymes of *A. thaliana* are indicated by bold arrows labelled with β or ε respectively. A bar below the arrow leading to ε-carotene indicates that the enzymatic

activity was examined but no product was detected. The steps marked by an arrow with a dotted line have not been specifically examined. Conventional numbering of the carbon atoms is given for neurosporene and α-carotene. Inverted triangles (▼) mark positions of the double bonds introduced as a consequence of the desaturation reactions.

Figure 3 depicts the carotene endgroups which are found in plants.

Figure 4 is a DNA sequence and the predicted amino acid sequence of a lycopene ε-cyclase cDNA isolated from *A. thaliana* (SEQ ID NOS: 1 and 2). These sequences were deposited under Genbank accession number U50738. This cDNA is incorporated into the plasmid pATeps.

Figure 5 is a DNA sequence encoding the β-carotene hydroxylase isolated from *A. thaliana* (SEQ ID NO: 3). This cDNA is incorporated into the plasmid pATOHB.

Figure 6 is an alignment of the predicted amino acid sequences of *A. thaliana* β-carotene hydroxylase (SEQ ID NO: 4) with those of the bacterial β-carotene hydroxylase enzymes from *Alicalgenes sp.* (SEQ ID NO: 5) (Genbank D58422), *Erwinia herbicola* Eho10 (SEQ ID NO.: 6) (GenBank M872280), *Erwinia uredovora* (SEQ ID NO.: 7) (GenBank D90087) and *Agrobacterium aurianticum* (SEQ ID NO.: 8) (GenBank D58420). A consensus sequence is also shown. All five genes are identical where a capital letter appears in the consensus. A lowercase letter indicates that three of five, including *A. thaliana*, have the identical residue. TM; transmembrane.

Figure 7 is a DNA sequence of a cDNA encoding an IPP isomerase isolated from *A. thaliana* (SEQ ID NO: 9). This cDNA is incorporated into the plasmid pATDP5.

Figure 8 is a DNA sequence of a second cDNA encoding another IPP isomerase isolated from *A. thaliana* (SEQ ID NO: 10). This cDNA is incorporated into the plasmid pATDP7.

Figure 9 is a DNA sequence of a cDNA encoding an IPP isomerase isolated from *Haematococcus pluvialis* (SEQ ID NO: 11). This cDNA is incorporated into the plasmid pHP04.

Figure 10 is a DNA sequence of a second cDNA encoding another IPP isomerase isolated from *Haematococcus pluvialis* (SEQ ID NO: 12). This cDNA is incorporated into the plasmid pHP05.

Figure 11 is an alignment of the amino acid sequences predicted by IPP isomerase cDNAs isolated from *A. thaliana (SEQ ID NO.: 16 and 18), H. pluvialis (SEQ ID NOS.: 14*

and 15), Clarkia breweri (SEQ ID NO.: 17) (See, Blanc & Pichersky, Plant Physiol. (1995) 108:855; Genbank accession no. X82627) and *Saccharomyces cerevisiae* (SEQ ID NO.: 19) (Genbank accession no. J05090).

Figure 12 is a DNA sequence of the cDNA encoding an IPP isomerase isolated from *Tagetes erecta* (marigold; SEQ ID NO: 13). This cDNA is incorporated into the plasmid pPMDP1. xxx's denote a region not originally sequenced. Figure 21A shows the complete marigold sequence.

Figure 13 is an alignment of the consensus sequence of four plant β-cyclases (SEQ ID NO.: 20) with the *A. thaliana* lycopene ε-cyclase (SEQ ID NO.: 21). A capital letter in the plant β consensus is used where all four β-cyclase genes predict the same amino acid residue in this position. A small letter indicates that an identical residue was found in three of the four. Dashes indicate that the amino acid residue was not conserved and dots in the sequence denote a gap. A consensus for the aligned sequences is given, in capital letters below the alignment, where the β- and ε-cyclases have the same amino acid residue. Arrows indicate some of the conserved amino acids that will be used as junction sites for construction of chimeric cyclases with novel enzymatic activities. Several regions of interest including a sequence signature indicative of a dinucleotide-binding motif and two predicted transmembrane (TM) helical regions are indicated below the alignment and are underlined.

Figure 14 shows the nucleotide (SEQ ID NO:22) and amino acid sequences (SEQ ID NO:23) of the *Adonis palaestina* (pheasant's eye) ε-cyclase cDNA #5.

Figure 15A shows the nucleotide (SEQ ID NO:24) and amino acid sequences (SEQ ID NO:25) of a potato ε-cyclase cDNA. Figure 15B shows the amino acid sequence (SEQ ID NO:26) of a chimeric lettuce/potato lycopene ε-cyclase. Amino acids in lower case are from the lettuce cDNA and those in upper case are from the potato cDNA. The product of this chimeric cDNA has e-cyclase activity and converts lycopene to the monocyclic δ-carotene.

Figure 16 shows a comparison between the amino acid sequences of the *Arabidopsis* ε-cyclase (SEQ ID NO:27) and the potato ε-cyclase (SEQ ID NO:25).

Figure 17A shows the nucleotide sequence of the *Adonis palaestina* Ipi1 (SEQ ID NO:28) and Figure 17B shows the nucleotide sequence of the *Adonis palaestina* Ipi2 (SEQ ID NO: 29).

Figure 18A shows the nucleotide sequence of the *Haematococcus pluvialis* Ipi1 (SEQ ID NO:11) and Figure 18B shows the nucleotide sequence of the *Haematococcus pluvialis* Ipi2 (SEQ ID NO:30).

Figure 19A shows the nucleotide sequence of the *Lactuca sativa (romaine lettuce)* Ipi1 (SEQ ID NO:31) and Figure 19B shows the nucleotide sequence of the *Lactuca sativa* Ipi2 (SEQ ID NO: 32).

Figure 20 shows the nucleotide sequence of the *Chlamydomonas reinhardtii* Ipi1 (SEQ ID NO:33).

Figure 21A shows the nucleotide sequence of the *Tagetes erecta* (marigold) Ipi1 (SEQ ID NO:34) and Figure 21B shows the nucleotide sequence of the *Oryza sativa* (rice) Ipi1 (SEQ ID NO:35).

Figure 22 shows a amino acid sequence alignment of various plant and green algal isopentenyl isomerases (IPI) (SEQ ID NOS:16, 36-45).

Figure 23 shows a comparison between *Adonis palaestina* ϵ-cyclase cDNA #3 and cDNA #5 nucleotide sequences.

Figure 24 shows a comparison between *Adonis palaestina* ϵ-cyclase cDNA #3 and cDNA #5 predicted amino acid sequences.

Figure 25 shows a sequence alignment of various plant β- and ϵ-cyclases. Those sequences outlined in grey denote identical sequences among the ϵ-cyclases. Those sequences outlined in black denote identical sequences among both the β- and ϵ-cyclases.

Figure 26 shows a sequence alignment of the plant ϵ-cyclases from Figure 25. Those sequences outlined in black denote identical sequences among the ϵ-cyclases.

Figure 27 is a dendrogram or "tree" illustrating the degree of amino acid sequence similarity for various lycopene β- and ϵ-cyclases.

Figure 28 shows a comparison between Arabidopsis ϵ-cyclase and lettuce ϵ-cyclase predicted amino acid sequences.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention includes an isolated and/or purified nucleic acid sequence which encodes for a protein having lycopene ϵ-cyclase, IPP isomerase or β-carotene hydroxylase enzyme activity and having the amino acid sequence of SEQ ID NOS: 2, 4, 14-21, 23 or 25-27. Nucleic acids encoding lycopene ϵ-cyclase, β-carotene hydroxylase and IPP

isomerases have been isolated from several genetically distant sources.

The present inventors have isolated nucleic acids encoding the enzyme IPP isomerase, which catalyzes the reversible conversion of isopentenyl pyrophosphate (IPP) to dimethylallyl pyrophosphate (DMAPP). IPP isomerase cDNAs were isolated from the plants *A. thaliana, Tagetes erecta* (marigold), *Adonis palaestina* (pheasant's eye), *Lactuca sativa* (romaine lettuce) and from the green algae *H. pluvialis* and *Chlamydomonas reinhardtii*. Alignments of the amino acid sequences predicted by some of these cDNAs are shown in Figures 12 and 22. Plasmids containing some of these cDNAs were deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville MD 20852 on March 4, 1996 under ATCC accession numbers 98000 (pHP05 - *H. pluvialis*); 98001 (pMDP1 - marigold); 98002 (pATDP7 - *A. thaliana*) and 98004 (pHP04 - *H. pluvialis*).

The present inventors have also isolated nucleic acids encoding the enzyme β-carotene hydroxylase, which is responsible for hydroxylating the β-endgroup in carotenoids. The nucleic acid of the present invention is shown in SEQ ID NO: 3 and Figure 5. The full length cDNA product hydroxylates both end groups of β-carotene as do products of cDNAs which encode proteins truncated by up to 50 amino acids from the N-terminus. Products of genes which encode proteins truncated between about 60-110 amino acids from the N-terminus preferentially hydroxylate only one ring. A plasmid containing this gene was deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville MD 20852 on March 4, 1996 under ATCC accession number 98003 (pATOHB - *A. thaliana*).

The present inventors have also isolated nucleic acids encoding the enzyme lycopene ϵ-cyclase, which is responsible for the formation of ϵ-endgroups in carotenoids. The *A. thaliane* ϵ-cyclase adds an ϵ ring to only one end of the symmetrical lycopene while the related β-cyclase adds a ring at both ends. The *A. thaliana* cDNA of the present invention is shown in Figure 4 and SEQ ID NO: 1. A plasmid containing this gene was deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville MD 20852 on March 4, 1996 under ATCC accession number 98005 (pATeps - *A. thaliana*).

In addition, lycopene ϵ-cyclases have been identified in lettuce and in *Adonis palaestina* (cDNA #5) which encode enzymes that convert lycopene to the bicyclic ϵ-carotene (ε,ε-carotene). An additional cDNA from *Adonis palaestina* (cDNA #3) encodes a lycopene ϵ-cyclase which converts lycopene into δ-carotene (ϵ,ψ-carotene) and differs from the lycopene ϵ-cyclase which forms bicyclic ϵ-carotene (ϵ,ϵ-carotene) by only 5 amino acids.

One or more of these amino acids may be modified by alteration of the nucleotide sequence in the #5 cDNA to obtain an enzyme which forms the bicyclic ϵ,ϵ-carotene. The sequences of the *Adonis palaestina* and *Arabidopsis thaliana* ϵ-cyclases have about 70% nucleotide identity and about 72% amino acid identity.

Initial experiments by the inventors with chimeric genes indicated that the part of the ϵ-cyclase which is responsible for adding 2 ϵ rings to form ϵ,ϵ-carotene is the carboxy terminal portion of the gene. The lettuce ϵ-cyclase adds two ϵ rings to form ϵ,ϵ-carotene. A DNA encoding a partial potato ϵ-cyclase (missing its amino terminal portion), when combined with an amino terminal region from the lettuce ϵ-cyclase gene, produces a monocyclic δ-carotene (ϵ,ψ-carotene). With the discovery of the differences between the *Adonis palaestina* clone #3 and clone #5, the specific amino acids responsible for the addition of an extra ϵ ring have been identified (Figure 24). Specifically, amino acid 55 is Thr in clone #3 and Ser in clone #5, amino acid 210 is Asn in clone #3 and Asp in clone #5, amino acid 231 is Asp in clone #3 and Glu in clone #5, amino acid 352 is Ile in clone #3 and Val in clone #5, and amino acid 524 is Lys in clone #3 and Arg in clone #5. It can be appreciated that these changes are quite conservative, as only one change, at amino acid 210, changes the charge of the protein.

Thus, it is clear that the nucleic acids of the invention encoding the enzymes as presently disclosed may be altered to increase a particularly desirable property of the enzyme, to change a property of the enzyme, or to diminish an undesirable property of the enzyme. Such modifications can be by deletion, substitution, or insertion of one or more amino acids, and can be performed by routine enzymatic manipulation of the nucleic acid encoding the enzyme (such as by restriction enzyme digestion, removal of nucleotides by mung bean nuclease or *Bal*31, insertion of nucleotides by Klenow fragment, and by religation of the ends), by site-directed mutagenesis, or may be accidental, such as by low fidelity PCR or those obtained through mutations in hosts that are producers of the enzymes. These techniques as well as other suitable techniques are well known in the art.

Mutations can be made in the nucleic acids of the invention such that a particular codon is changed to a codon which codes for a different amino acid. Such a mutation is generally made by making the fewest nucleotide changes possible. A substitution mutation of this sort can be made to change an amino acid in the resulting protein in a non-conservative manner (i.e., by changing the codon from an amino acid belonging to a grouping

of amino acids having a particular size or characteristic to an amino acid belonging to another grouping) or in a conservative manner (i.e., by changing the codon from an amino acid belonging to a grouping of amino acids having a particular size or characteristic to an amino acid belonging to the same grouping). Such a conservative change generally leads to less change in the structure and function of the resulting protein. A non-conservative change is more likely to alter the structure, activity or function of the resulting protein. The present invention should be considered to include sequences containing conservative changes which do not significantly alter the activity or binding characteristics of the resulting protein.

The following is one example of various groupings of amino acids:

Amino acids with nonpolar R groups: Alanine, Valine, Leucine, Isoleucine, Proline, Phenylalanine, Tryptophan and Methionine.

Amino acids with uncharged polar R groups: Glycine, Serine, Threonine, Cysteine, Tyrosine, Asparagine and Glutamine.

Amino acids with charged polar R groups (negatively charged at Ph 6.0): Aspartic acid and Glutamic acid.

Basic amino acids (positively charged at pH 6.0): Lysine, Arginine and Histidine.

Another grouping may be those amino acids with phenyl groups: Phenylalanine, Tryptophan and Tyrosine.

Another grouping may be according to molecular weight (i.e., size of R groups).

Particularly preferred substitutions are:

- Lys for Arg and vice versa such that a positive charge may be maintained;
- Glu for Asp and vice versa such that a negative charge may be maintained;
- Ser for Thr such that a free -OH can be maintained; and
- Gln for Asn such that a free NH_2 can be maintained.

Amino acid substitutions may also be introduced to substitute an amino acid with a particularly preferable property. For example, a Cys may be introduced to provide a potential site for disulfide bridges with another Cys. A His may be introduced as a particularly "catalytic" site (i.e., His can act as an acid or base and is the most common amino acid in biochemical catalysis). Pro may be introduced because of its particularly planar structure, which induces β-turns in the protein's structure.

It is clear that certain modifications of SEQ ID NOS: 2, 4, 14-21, 23 or 25-27 can take place without destroying the activity of the enzyme. It is noted especially that truncated

versions of the nucleic acids of the invention are functional. For example, several amino acids (from 1 to about 120) can be deleted from the N-terminus of the lycopene ϵ-cyclases of the invention, and a functional protein can still be produced. This fact is made especially clear from Figure 25, which shows a sequence alignment of several plant ϵ-cyclases. As can be seen from Figure 25, there is an enormous amount of sequence disparity between amino acid sequences 2 to about 50-70 (depending on the particular sequence, since gaps are present). There is less, but also a substantial amount of, sequence dissimilarity between about 50-70 to about 90-120 (depending on the particular sequence). Thereafter, the sequences are fairly conserved, except for small pockets of dissimilarity between about 275-295 to about 285-305 (depending on the particular sequence), and between about 395-415 to about 410-430 (depending on the particular sequence).

The present inventors have found that the amount of the 5' region present in the nucleic acids of the invention can alter the activity of the enzyme. Instead of diminishing activity, truncating the 5' region of the nucleic acids of the invention may result in an enzyme with a different specificity. Thus, the present invention relates to nucleic acids and enzymes encoded thereby which are truncated to within 0-50, preferably 0-25, codons of the 5' initiation codon of their prokaryotic counterparts as determined by alignment maps as discussed below.

For example, when the cDNA encoding *A. thaliana* β-carotene hydroxylase was truncated, the resulting enzyme catalyzed the formation of β-cryptoxanthin as the major product and zeaxanthin as minor product; in contrast to its normal production of zeaxanthin.

The present invention is intended to include those nucleic acid and amino acid sequences in which substitutions, deletions, additions or other modifications have taken place, as compared to SEQ ID NOS: 2, 4, 14-21, 23 or 25-27, without destroying the activity of the enzyme. Preferably, the substitutions, deletions, additions or other modifications take place at the 5' end, or any other of those positions which already show dissimilarity between any of the presently disclosed amino acid sequences (see also Figure 25) or other amino acid sequences which are known in the art and which encode the same enzyme (i.e., lycopene ϵ-cyclase, IPP isomerase or β-carotene hydroxylase).

In each case, nucleic acid and amino acid sequence similarity and identity is measured using sequence analysis software, for example, the Sequence Analysis, Gap, or BestFit software packages of the Genetics Computer Group (University of Wisconsin Biotechnology

Center, 1710 University Avenue, Madison, Wisconsin 53705), MEGAlign (DNAStar, Inc., 1228 S. Park St., Madison, Wisconsin 53715), or MacVector (Oxford Molecular Group, 2105 S. Bascom Avenue, Suite 200, Campbell, California 95008). Such software uses algorithms to match similar sequences by assigning degrees of identity to various substitutions, deletions, and other modifications, and includes detailed instructions as to useful parameters, etc., such that those of routine skill in the art can easily compare sequence similarities and identities. An example of a useful algorithm in this regard is the algorithm of Needleman and Wunsch, which is used in the Gap program discussed above. This program finds the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. Another useful algorithm is the algorithm of Smith and Waterman, which is used in the BestFit program discussed above. This program creates an optimal alignment of the best segment of similarity between two sequences. Optimal alignments are found by inserting gaps to maximize the number of matches using the local homology algorithm of Smith and Waterman.

Conservative (i.e. similar) substitutions typically include substitutions within the following groups: glycine and alanine; valine, isoleucine and leucine; aspartic acid, glutamic acid, asparagine and glutamine; serine and threonine; lysine and arginine; and phenylalanine and tyrosine. Substitutions may also be made on the basis of conserved hydrophobicity or hydrophilicity (see Kyte and Doolittle, *J. Mol. Biol.* **157**: 105-132 (1982)), or on the basis of the ability to assume similar polypeptide secondary structure (see Chou and Fasman, *Adv. Enzymol.* **47**: 45-148 (1978)).

If comparison is made between nucleotide sequences, preferably the length of comparison sequences is at least 50 nucleotides, more preferably at least 60 nucleotides, at least 75 nucleotides or at least 100 nucleotides. It is most preferred if comparison is made between the nucleic acid sequences encoding the enzyme coding regions necessary for enzyme activity. If comparison is made between amino acid sequences, preferably the length of comparison is at least 20 amino acids, more preferably at least 30 amino acids, at least 40 amino acids or at least 50 amino acids. It is most preferred if comparison is made between the amino acid sequences in the enzyme coding regions necessary for enzyme activity.

It should be appreciated that also within the scope of the present invention are nucleic acid sequences encoding lycopene ε-cyclases, IPP isomerases and β-carotene hydroxylases

which code for enzymes having the same amino acid sequence as SEQ ID NOS: 2, 4, 14-21, 23 or 25-27, but which are degenerate to the nucleic acids specifically disclosed herein.

The amino acid residues described herein are preferred to be in the "L" isomeric form. However, residues in the "D" isomeric form can be substituted for any L-amino acid residue, as long as the desired functional property of immunoglobulin-binding is retained by the polypeptide.

In accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook et al, "Molecular Cloning: A Laboratory Manual" (1989); "Current Protocols in Molecular Biology" Volumes I-III [Ausubel, R. M., ed. (1994)]; "Cell Biology: A Laboratory Handbook" Volumes I-III [J. E. Celis, ed. (1994))]; "Current Protocols in Immunology" Volumes I-III [Coligan, J. E., ed. (1994)]; "Oligonucleotide Synthesis" (M.J. Gait ed. 1984); "Nucleic Acid Hybridization" [B.D. Hames & S.J. Higgins eds. (1985)]; "Transcription And Translation" [B.D. Hames & S.J. Higgins, eds. (1984)]; "Animal Cell Culture" [R.I. Freshney, ed. (1986)]; "Immobilized Cells And Enzymes" [IRL Press, (1986)]; B. Perbal, "A Practical Guide To Molecular Cloning" (1984).

The present invention also includes vectors. Suitable vectors according to the present invention comprise a nucleic acid of the invention encoding an enzyme involved in carotenoid biosynthesis or metabolism and a suitable promoter for the host, and can be constructed using techniques well known in the art (for example Sambrook et al., Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989; Ausubel et al., Current Protocols in Molecular Biology, Greene Publishing and Wiley Interscience, New York, 1991). Suitable vectors for eukaryotic expression in plants are described in Frey et al., Plant J. (1995) 8(5):693 and Misawa et al, 1994a; incorporated herein by reference. Suitable vectors for prokaryotic expression include pACYC184, pUC119, and pBR322 (available from New England BioLabs, Bevery, MA) and pTrcHis (Invitrogen) and pET28 (Novagen) and derivatives thereof. The vectors of the present invention can additionally contain regulatory elements such as promoters, repressors, selectable markers such as antibiotic resistance genes, etc.

The nucleic acids encoding the carotenoid enzymes as described above, when cloned into a suitable expression vector, can be used to overexpress these enzymes in a plant

expression system or to inhibit the expression of these enzymes. For example, a vector containing the gene encoding lycopene ϵ-cyclase can be used to increase the amount of α-carotene and carotenoids derived from α-carotene (such as lutein and α-cryptoxanthin) in an organism and thereby alter the nutritional value, pharmacology and visual appearance value of the organism.

Therefore, the present invention includes a method of producing or enhancing the production of a carotenoid in a host cell, relative to an untransformed host cell, the method comprising inserting into the host cell a vector comprising a heterologous nucleic acid sequence which encodes for a protein having lycopene ϵ-cyclase, IPP isomerase or β-carotene hydroxylase enzyme activity, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence to produce the protein.

The present invention also includes a method of modifying the production of carotenoids in a host cell, the method comprising inserting into the host cell a vector comprising a heterologous nucleic acid sequence which produces an RNA and/or encodes for a protein which modifies lycopene ϵ-cyclase, IPP isomerase or β-carotene hydroxylase enzyme activity, relative to an untransformed host cell, wherein the heterologous nucleic acid sequence is operably linked to a promoter; and expressing the heterologous nucleic acid sequence in the host cell to modify the production of the carotenoids in the host cell, relative to the untransformed host cell.

The term "modifying the production" means that the amount of carotenoids produced in the host cell can be enhanced, reduced, or left the same, as compared to the untransformed host cell. In accordance with one embodiment of the present invention, the make-up of the carotenoids (i.e., the specific carotenoids produced) is changed *vis a vis* each other, and this change in make-up may result in either a net gain, net loss, or no net change in the total amount of carotenoids produced in the cell. In accordance with another embodiment of the present invention, the production or the biochemical activity of the carotenoids (or the enzymes which catalyze their formation) is enhanced by the insertion of an enzyme-encoding nucleic acid of the invention. In yet another embodiment of the invention, the production or the biochemical activity of the carotenoids (or the enzymes which catalyze their formation) may be reduced or inhibited by a number of different approaches available to those skilled in the art, including but not limited to such methodologies or approaches as anti-sense (e.g.,

Gray et al (1992) Plant Mol. Biol. 19:69-87), ribozymes (e.g., Wegener et al (1994) Mol. Gen. Genet. 245:465-470), co-suppression (e.g., Fray and Grierson (1993) Plant Mol. Biol. 22:589-602), targeted disruption of the gene (e.g., Schaefer et al. (1997) Plant J. 11:1195-1206), intracellular antibodies (e.g., Rondon and Marasco (1997) Ann. Rev. Microbiol. 51:257-283) or whatever other approaches rely on the knowledge or availability of the nucleic acid or amino acid sequences of the invention and/or portions thereof, to thereby reduce accumulation of carotenoids with ϵ rings and compounds derived from them (for ϵ-cyclase inhibition), or carotenoids with hydroxylated β rings and compounds derived from them (for β-hydroxylase inhibition), or, in the case if IPP isomerase, accumulation of any isoprenoid compound.

Preferably, at least a portion of the nucleic acid sequences used in the methods, vectors and host cells of the invention codes for an enzyme having an amino acid sequence which is at least 85% identical, preferably at least 90%, at least 95% or completely identical to SEQ ID NOS: 2, 4, 14-21, 23 or 25-27. Sequence identity is determined as noted above. Preferably, sequence additions, deletions or other modifications are made as indicated above, so as to not affect the function of the particular enzyme.

In a preferred embodiment, vectors are manufactured which contain a DNA encoding a eukaryotic IPP isomerase upstream of a DNA encoding a second eukaryotic carotenoid enzyme. The inventors have discovered that inclusion of an IPP isomerase gene increases the supply of substrate for the carotenoid pathway; thereby enhancing the production of carotenoid endproducts, as compared to a host cell which is not transformed with such a vector. This is apparent from the much deeper pigmentation in carotenoid-accumulating colonies of *E. coli* which also contain one of the aforementioned IPP isomerase genes when compared to colonies that lack this additional IPP isomerase gene. Similarly, a vector comprising an IPP isomerase gene can be used to enhance production of any secondary metabolite of dimethylallyl pyrophosphate and/or isopentenyl pyrophosphate (such as isoprenoids, steroids, carotenoids, etc.). The term "isoprenoid" is intended to mean any member of the class of naturally occurring compounds whose carbon skeletons are composed, in part or entirely, of isopentyl C_5 units. Preferably, the carbon skeleton is of an essential oil, a fragrance, a rubber, a carotenoid, or a therapeutic compound, such as paclitaxel.

A vector containing the cDNA encoding a lycopene ϵ-cyclase of the invention, preferably the lettuce lycopene ϵ-cyclase or Adonis ϵ-cyclase #5, can be used to increase the

amount of bicyclic ϵ-carotene in an organism and thereby alter the nutritional value, pharmacology and visual appearance value of the organism. In addition, the transformed organism can be used in the formulation of therapeutic agents, for example in the treatment of cancer (see Mayne et al (1996) FASEB J. 10:690-701; Tsushima et al (1995) Biol. Pharm. Bull. 18:227-233).

An antisense strand of a nucleic acid of the invention can be inserted into a vector. For example, the lycopene ϵ-cyclase gene can be inserted into a vector and incorporated into the genomic DNA of a host, thereby inhibiting the synthesis of ϵ,β-carotenoids (lutein and α-carotene) and enhancing the synthesis of β,β-carotenoids (zeaxanthin and β-carotene).

The present invention also relates to novel enzymes which are encoded by the amino acid sequences of the invention, or portions thereof.

The present invention also relates to novel enzymes which can transform known carotenoids into novel or uncommon products. Currently ϵ-carotene (see Figure 2) and γ-carotene are commonly produced only in minor amounts. As described below, an enzyme can be produced which transforms lycopene to γ-carotene and lycopene to ϵ-carotene. With these products in hand, bulk synthesis of other carotenoids derived from them are possible. For example, ϵ-carotene can be hydroxylated to form lactucaxanthin, an isomer of lutein (one ϵ and one β ring) and zeaxanthin (two β rings) where both endgroups are, instead, ϵ rings.

In addition to novel enzymes produced by truncating the 5' region of known enzymes, as discussed above, novel enzymes which can participate in the formation of unusual carotenoids can be formed by replacing portions of one gene with an analogous sequence from a structurally related gene. For example, β-cyclase and ϵ-cyclase are structurally related (see Figure 13). By replacing a portion of β-lycopene cyclase with the analogous portion of ϵ-cyclase, an enzyme which produces γ-carotene will be produced (one β endgroup). Further, by replacing a portion of the lycopene ϵ-cyclase with the analogous portion of β-cyclase, an enzyme which produces ϵ-carotene will be produced (with some exceptions, such as the lettuce ε-cyclase, plant ϵ-cyclases normally produce a compound with one ϵ-endgroup, δ-carotene). Similarly, β-hydroxylase could be modified to produce enzymes of novel function by creation of hybrids with ϵ-hydroxylase.

Host systems according to the present invention can comprise any organism that already produces carotenoids or which has been genetically modified to produce carotenoids.

The IPP isomerase genes are more broadly applicable for enhancing production of any product dependent on DMAPP and/or IPP as a precursor.

Organisms which already produce carotenoids include plants, algae, some yeasts, fungi and cyanobacteria and other photosynthetic bacteria. Transformation of these hosts with vectors according to the present invention can be done using standard techniques such as those described in Misawa et al., (1990) supra; Hundle et al., (1993) supra; Hundle et al., (1991) supra; Misawa et al., (1991) supra; Sandmann et al., supra; and Schnurr et al., supra.

Transgenic organisms can be constructed which include the nucleic acid sequences of the present invention (Bird et al, 1991; Bramley et al, 1992; Misawa et al, 1994a; Misawa et al, 1994b; Cunningham et al, 1993). The incorporation of these sequences can allow the controlling of carotenoid biosynthesis, content, or composition in the host cell. These transgenic systems can be constructed to incorporate sequences which allow for the overexpression of the nucleic acids of the present invention. Transgenic systems can also be constructed containing antisense expression of the nucleic acid sequences of the present invention. Such antisense expression would result in the accumulation of the substrates of the substrates of the enzyme encoded by the sense strand.

A method for screening for eukaryotic genes which encode enzymes involved in carotenoid biosynthesis comprises transforming a prokaryotic host with a nucleic acid which may contain a eukaryotic or prokaryotic carotenoid biosynthetic gene; culturing said transformed host to obtain colonies; and screening for colonies exhibiting a different color than colonies of the untransformed host.

Suitable hosts include *E. coli,* cyanobacteria such as *Synechococcus* and *Synechocystis,* alga and plant cells. *E. coli* are preferred.

In a preferred embodiment, the above "color complementation" screening protocol can be enhanced by using mutants which are either (1) deficient in at least one carotenoid biosynthetic gene or (2) overexpress at least one carotenoid biosynthetic gene. In either case, such mutants will accumulate carotenoid precursors.

Prokaryotic and eukaryotic DNA or cDNA libraries can be screened in total for the presence of genes of carotenoid biosynthesis, metabolism and degradation. Preferred organisms to be screened include photosynthetic organisms.

E. coli can be transformed with these eukaryotic cDNA libraries using conventional methods such as those described in Sambrook et al, 1989 and according to protocols described by the vendors of the cloning vectors.

For example, the cDNA libraries in bacteriophage vectors such as lambdaZAP (Stratagene) or lambda ZIPLOX (Gibco BRL) can be excised en masse and used to transform *E.coli*.

Transformed *E. coli* can be cultured using conventional techniques. The culture broth preferably contains antibiotics to select and maintain plasmids. Suitable antibiotics include penicillin, ampicillin, chloramphenicol, etc. Culturing is typically conducted at 15-40°C, preferably at room temperature or slightly above (18-28°C), for 12 hours to 7 days.

Cultures are plated and the plates are screened visually for colonies with a different color than the colonies of the host *E. coli* transformed with the empty plasmid cloning vector. For example, *E. coli* transformed with the plasmid, pAC-BETA (described below), produce yellow colonies that accumulate β-carotene. After transformation with a cDNA library, colonies which contain a different hue than those formed by *E. coli*/pAC-BETA would be expected to contain enzymes which modify the structure or accumulation of β-carotene. Similar E. coli strains can be engineered which accumulate earlier products in carotenoid biosynthesis, such as lycopene, γ-carotene, etc.

Having generally described this invention, a further understanding can be obtained by reference to certain specific examples which are provided herein for purposes of illustration only and are not intended to be limiting unless otherwise specified.

EXAMPLE

I. Isolation of β-carotene hydroxylase

Plasmid Construction

An 8.6kb BglII fragment containing the carotenoid biosynthetic genes of *Erwinia herbicola* was first cloned in the BamHI site of plasmid vector pACYC184 (chloramphenicol resistant), and then a 1.1kb BamHI fragment containing the *E. herbicola* β-carotene hydroxylase (*CrtZ*) was deleted. *E.coli* strains containing the resulting plasmid, pAC-BETA, accumulate ß-carotene and form yellow colonies (Cunningham et al., 1994).

A full length cDNA encoding IPP isomerase of *Haematococcus pluvialis* (HP04) was first excised with *BamH*I and *Kpn*I from pBluescript SK-, and then ligated into the

corresponding sites of the pTrcHisA vector with high-level expression from the *trc* promoter (Invitrogen, Inc.). A fragment containing the IPP isomerase and *trc* promoter was subsequently excised with *EcoR*V and *Kpn*I, treated with the Klenow fragment of DNA polymerase to produce blunt ends, and ligated in the Klenow-treated *Hind*III site of pAC-BETA. *E.coli* cells transformed with this new plasmid pAC-BETA-04 form orange colonies on LB plates (*vs.* yellow for those containing pAC-BETA) and cultures accumulate substantially more β-carotene (*ca.* two fold) than those that contain pAC-BETA.

Screening of an Arabidopsis cDNA Library

Several λ cDNA expression libraries of *Arabidopsis* were obtained from the *Arabidopsis* Biological Resource Center (Ohio State University, Columbus, OH) (Kieber et al., 1993). The λ cDNA libraries were excised *in vivo* using Stratagene's ExAssist SOLR system to produce a phagemid cDNA library wherein each phagemid contained also a gene conferring resistance to the antibiotic ampicillin.

E.coli strain DH10BZIP was chosen as the host cell for the screening and pigment production, although we have also used TOP10F' and XL1-Blue for this purpose. DH10B cells were transformed with plasmid pAC-BETA-04 and were plated on LB agar plates containing chloramphenicol at 50 μg/ml (from United States Biochemical Corporation). The phagemid *Arabidopsis* cDNA library was then introduced into DH10B cells already containing pAC-BETA-04. Transformed cells containing both pAC-BETA-04 and *Arabidopsis* cDNA library phagemids were selected on chloramphenicol plus ampicillin (150 μg/ml) agar plates. Maximum color development occurred after 3 to 7 days incubation at room temperature, and the rare bright yellow colonies were selected from a background of many thousands of orange colonies on each agar plate. Selected colonies were inoculated into 3 ml liquid LB medium containing ampicillin and chloramphenicol, and cultures were incubated at room temperature for 1-2 days, with shaking. Cells were then harvested by centrifugation and extracted with acetone in microfuge tubes. After centrifugation, the pigmented extract was spotted onto silica gel thin-layer chromatography (TLC) plates, and developed with a hexane:ether (1:1, by volume) mobile phases. ß-carotene hydroxylase-encoding cDNAs were identified based on the appearance of a yellow pigment that co-migrated with zeaxanthin on the TLC plates.

Subcloning and Sequencing

The plasmid containing the ß-carotene hydroxylase cDNA was recovered and analyzed by standard procedures (Sambrook et al., 1989). The *Arabidopsis* ß-carotene hydroxylase was sequenced completely on both strands on an automatic sequencer (Applied Biosystems, Model 373A, Version 2.0.1S). The cDNA insert of 0.95kb also was excised and ligated into the a pTrcHis vector. A *Bgl*II restriction site within the cDNA was used to remove that portion of the cDNA that encodes the predicted polypeptide N terminal sequence region that is not also found in bacterial β-carotene hydroxylases (Figure 6). A BglII-XhoI fragment was directionally cloned in BamHI-XhoI digested TrcHis vectors.

Pigment Analysis

A single colony was used to inoculate 50 ml of LB containing ampicillin and chloramphenicol in a 250-ml flask. Cultures were incubated at 28°C for 36 hours with gentle shaking, and then harvested at 5000 rpm in an SS-34 rotor. The cells were washed once with distilled H_2O and resuspended with 0.5 ml of water. The extraction procedures and HPLC were essentially as described previously (Cunningham et al, 1994).

II. Isolation and biochemical analysis of an Arabidopsis lycopene ϵ-cyclase

Plasmid Construction

Construction of plasmids pAC-LYC, pAC-NEUR, and pAC-ZETA is described in Cunningham et al., (1994). In brief, the appropriate carotenoid biosynthetic genes from *Erwinia herbicola*, *Rhodobacter capsulatus*, and *Synechococcus* sp. strain PCC7942 were cloned in the plasmid vector pACYC184 (New England BioLabs, Beverly, MA). Cultures of *E. coli* containing the plasmids pAC-ZETA, pAC-NEUR, and pAC-LYC, accumulate ζ-carotene, neurosporene, and lycopene, respectively. The plasmid pAC-ZETA was constructed as follows: an 8.6-kb BglII fragment containing the carotenoid biosynthetic genes of *E. herbicola* (GenBank M87280; Hundle et al., 1991) was obtained after partial digestion of plasmid pPL376 (Perry et al., 1986; Tuveson et al., 1986) and cloned in the BamHI site of pACYC184 to give the plasmid pAC-EHER. Deletion of adjacent 0.8- and 1.1-kb BamHI-BamHI fragments (deletion Z in Cunningham et al., 1994), and of a 1.1 kB SalI-SalI fragment (deletion X) served to remove most of the coding regions for the *E. herbicola* β-carotene hydroxylase (crtZ gene) and zeaxanthin glucosyltransferase (crtX gene), respectively. The

resulting plasmid, pAC-BETA, retains functional genes for geranylgeranyl pyrophosphate synthase (crtE), phytoene synthase (crtB), phytoene desaturase (crtI), and lycopene cyclase (crtY). Cells of *E. coli* containing this plasmid form yellow colonies and accumulate β-carotene. A plasmid containing both the lycopene ϵ- and β-cyclase cDNAs of *A. thaliana* was constructed by excising the ϵ-cyclase in clone y2 as a PvuI-PvuII fragment and ligating this piece in the SnaBI site of a plasmid (pSPORT 1 from GIBCO-BRL) that already contained the β-cyclase (Cunningham et al., 1996).

Organisms and Growth Conditions

E. coli strains TOP10 and TOP10 F' (obtained from Invitrogen Corporation, San Diego, CA) and XL1-Blue (Stratagene) were grown in Luria-Bertani (LB) medium (Sambrook et al., 1989) at 37°C in darkness on a platform shaker at 225 cycles per min. Media components were from Difco (yeast extract and tryptone) or Sigma (NaCl). Ampicillin at 150 μg/mL and/or chloramphenicol at 50 μg/mL (both from United States Biochemical Corporation) were used, as appropriate, for selection and maintenance of plasmids.

Mass Excision and Color Complementation Screening of an *A. thaliana* cDNA Library

A size-fractionated 1-2 kB cDNA library of *A. thaliana* in lambda ZAPII (Kieber et al., 1993) was obtained from the Arabidopsis Biological Resource Center at The Ohio State University (stock number CD4-14). Other size fractionated libraries were also obtained (stock numbers CD4-13, CD4-15, and CD4-16). An aliquot of each library was treated to cause a mass excision of the cDNAs and thereby produce a phagemid library according to the instructions provided by the supplier of the cloning vector (Stratagene; *E. coli* strain XL1-Blue and the helper phage R408 were used). The titre of the excised phagemid was determined and the library was introduced into a lycopene-accumulating strain of *E. coli* TOP10 F' (this strain contained the plasmid pAC-LYC) by incubation of the phagemid with the *E. coli* cells for 15 min at 37°C. Cells had been grown overnight at 30°C in LB medium supplemented with 2% (w/v) maltose and 10 mM $MgSO_4$ (final concentration), and harvested in 1.5 ml microfuge tubes at a setting of 3 on an Eppendorf microfuge (5415C) for 10 min. The pellets were resuspended in 10 mM $MgSO_4$ to a volume equal to one-half that of the

initial culture volume. Transformants were spread on large (150 mm diameter) LB agar petri plates containing antibiotics to provide for selection of cDNA clones (ampicillin) and maintenance of pAC-LYC (chloramphenicol). Approximately 10,000 colony forming units were spread on each plate. Petri plates were incubated at 37·C for 16 hr and then at room temperature for 2 to 7 days to allow maximum color development. Plates were screened visually with the aid of an illuminated 3x magnifier and a low power stage-dissecting microscope for the rare, pale pinkish-yellow to deep-yellow colonies that could be observed in the background of pink colonies. A colony color of yellow or pinkish-yellow was taken as presumptive evidence of a cyclization activity. These yellow colonies were collected with sterile toothpicks and used to inoculate 3ml of LB medium in culture tubes with overnight growth at 37°C and shaking at 225 cycles/min. Cultures were split into two aliquots in microfuge tubes and harvested by centrifugation at a setting of 5 in an Eppendorf 5415C microfuge. After discarding the liquid, one pellet was frozen for later purification of plasmid DNA. To the second pellet was added 1.5 ml EtOH, and the pellet was resuspended by vortex mixing, and extraction was allowed to proceed in the dark for 15-30 min with occasional remixing. Insoluble materials were pelleted by centrifugation at maximum speed for 10 min in a microfuge. Absorption spectra of the supernatant fluids were recorded from 350-550 nm with a Perkin Elmer lambda six spectrophotometer.

<u>Analysis of isolated clones</u>

Eight of the yellow colonies contained β-carotene indicating that a single gene product catalyzes both cyclizations required to form the two β endgroups of the symmetrical β-carotene from the symmetrical precursor lycopene. One of the yellow colonies contained a pigment with the spectrum characteristic of δ-carotene, a monocyclic carotenoid with a single ϵ endgroup. Unlike the β cyclase, this ϵ-cyclase appears unable to carry out a second cyclization at the other end of the molecule.

The observation that ϵ-cyclase is unable to form two cyclic ϵ-endgroups (*e.g.* the bicyclic ϵ-carotene) illuminates the mechanism by which plants can coordinate and control the flow of substrate into carotenoids derived from β-carotene versus those derived from α-carotene and also can prevent the formation of carotenoids with two ϵ endgroups.

The availability of the *A. thaliana* gene encoding the ϵ-cyclase enables the directed manipulation of plant and algal species for modification of carotenoid content and

composition. Through inactivation of the ϵ-cyclase, whether at the gene level by deletion of the gene or by insertional inactivation or by reduction of the amount of enzyme formed (by such as antisense technology), one may increase the formation of β-carotene and other pigments derived from it. Since vitamin A is derived only from carotenoids with β endgroups, an enhancement of the production of β-carotene versus α-carotene may enhance nutritional value of crop plants. Reduction of carotenoids with ϵ-endgroups may also be of value in modifying the color properties of crop plants and specific tissues of these plants. Alternatively, where production of α-carotene, or pigments such as lutein that are derived from α-carotene, is desirable, whether for the color properties, nutritional value or other reason, one may overexpress the ϵ-cyclase or express it in specific tissues. Wherever agronomic value of a crop is related to pigmentation provided by carotenoid pigments the directed manipulation of expression of the ϵ-cyclase gene and/or production of the enzyme may be of commercial value.

The predicted amino acid sequence of the *A. thaliana* ϵ-cyclase enzyme was determined. A comparison of the amino acid sequences of the β- and ϵ-cyclase enzymes of *Arabidopsis thaliana* (Fig. 13) as predicted by the DNA sequence of the respective cDNAs (Fig. 4 for the ϵ-cyclase cDNA sequence), indicates that these two enzymes have many regions of sequence similarity, but they are only about 37% identical overall at the amino acid level. The degree of sequence identity at the DNA base level, only about 50%, is sufficiently low such that we and others have been unable to detect this gene by hybridization using the β cyclase as a probe in DNA gel blot experiments.

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Having now fully described the invention, it will be apparent to one of ordinary skill in the art that many changes and modifications can be made thereto without departing from the spirit or scope of the invention as set forth herein.

We claim:

1. An isolated and/or purified nucleic acid sequence which encodes for a protein having lycopene ϵ-cyclase enzyme activity and has an amino acid sequence which is at least 85% identical to one of SEQ ID NOS: 23 or 25-27.

2. The nucleic acid sequence of claim 1, wherein the protein has the amino acid sequence of one of SEQ ID NOS: 23 or 25-27.

3. A vector comprising the nucleic acid sequence of claim 1, wherein the nucleic acid sequence is operably linked to a promoter.

4. A host cell which contains the vector of claim 3.

5. The host cell of claim 4, wherein the host cell is selected from the group consisting of a bacterial cell, an algal cell, a yeast cell and a plant cell.

6. The host cell of claim 4, wherein the host cell is a photosynthetic cell.

7. An isolated and/or purified protein having lycopene ϵ-cyclase enzyme activity and having an amino acid sequence which is at least 85% identical to one of SEQ ID NOS: 23 or 25-27.

8. The protein of claim 7, wherein the protein has the amino acid sequence of one of SEQ ID NOS: 23 or 25-27.

AMENDED CLAIMS

[received by the International Bureau on 15 November 1999 (15.11.99); original claims 1,2,7 and 8 amended; remaining claims unchanged (1 page)]

1. An isolated and/or purified nucleic acid sequence which encodes for a protein having lycopene ϵ-cyclase enzyme activity and has an amino acid sequence which is at least 85% identical to one of SEQ ID NOS: 23, 25 or 26.

2. The nucleic acid sequence of claim 1, wherein the protein has the amino acid sequence of one of SEQ ID NOS: 23, 25 or 26.

3. A vector comprising the nucleic acid sequence of claim 1, wherein the nucleic acid sequence is operably linked to a promoter.

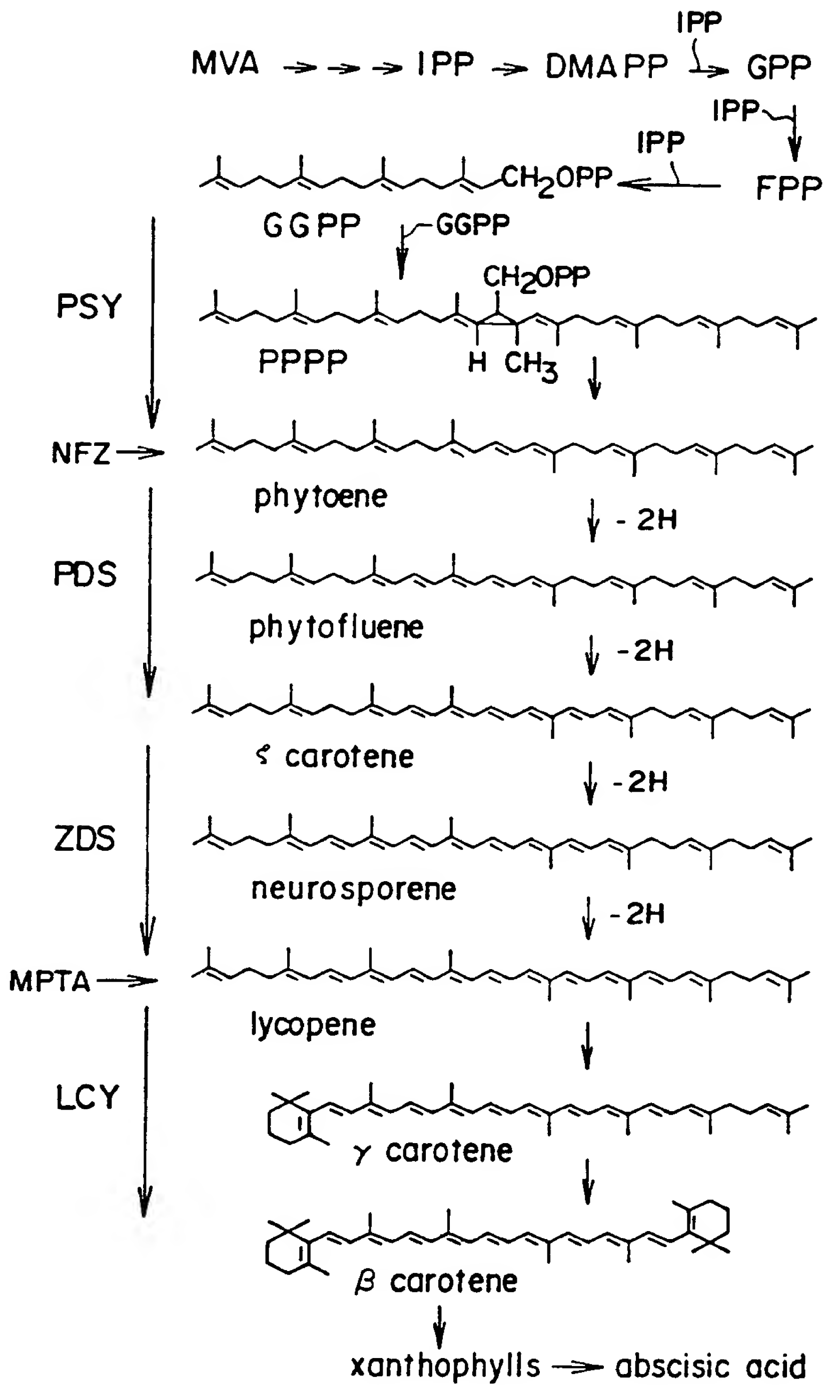
4. A host cell which contains the vector of claim 3.

5. The host cell of claim 4, wherein the host cell is selected from the group consisting of a bacterial cell, an algal cell, a yeast cell and a plant cell.

6. The host cell of claim 4, wherein the host cell is a photosynthetic cell.

7. An isolated and/or purified protein having lycopene ϵ-cyclase enzyme activity and having an amino acid sequence which is at least 85% identical to one of SEQ ID NOS: 23, 25 or 26.

8. The protein of claim 7, wherein the protein has the amino acid sequence of one of SEQ ID NOS: 23, 25 or 26.



MVA
IPP
DMAPP
IPP
GPP
IPP
IPP
FPP
CH2OPP
GGPP
GGPP
PSY
CH2OPP
PPPP
H CH3
NFZ
phytoene
- 2H
PDS
phytofluene
-2H
ζ carotene
-2H
ZDS
neurosporene
-2H
MPTA
lycopene
LCY
γ carotene
β carotene
xanthophylls
abscisic acid

FIG. 1

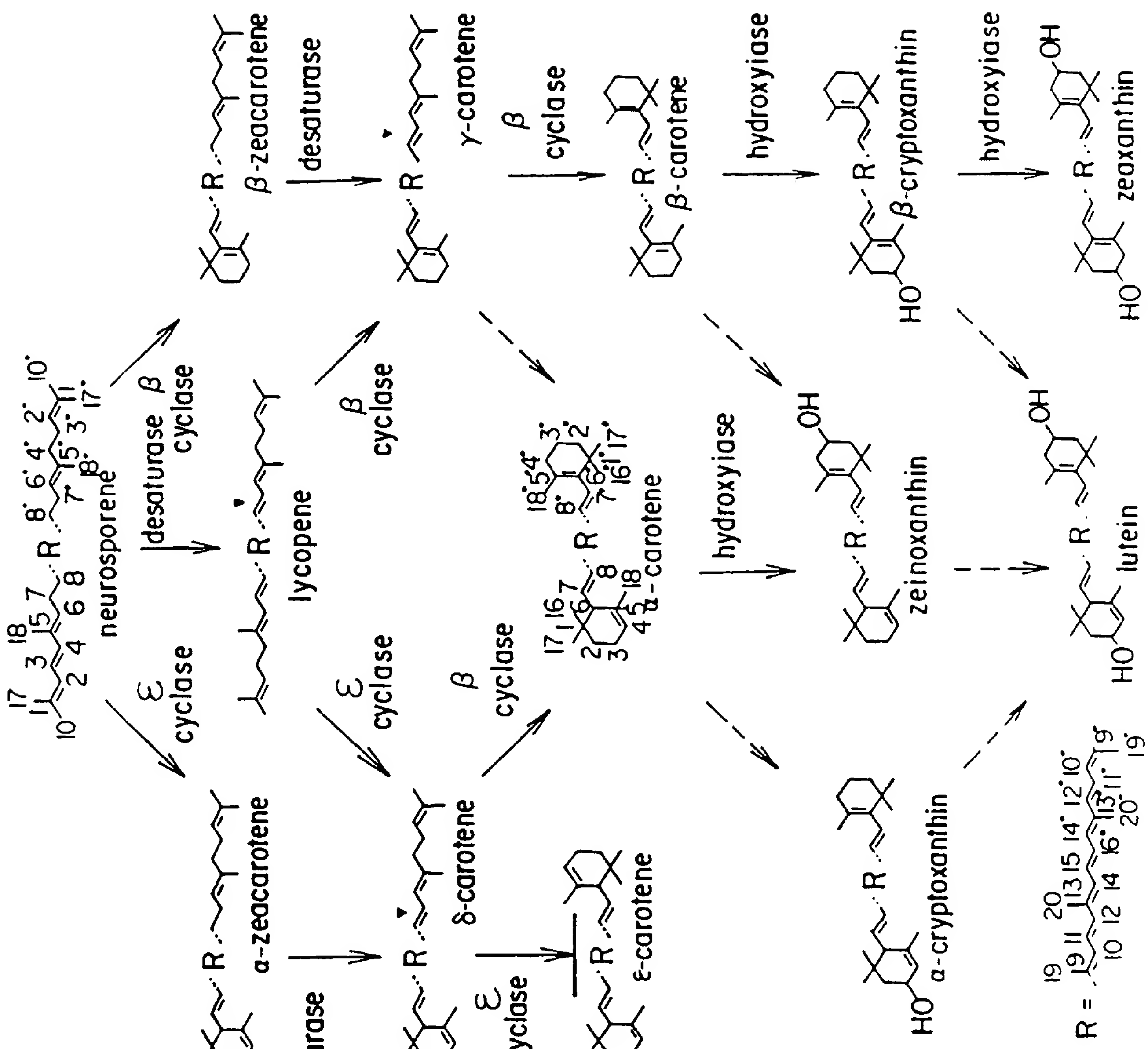

neurosporene
ε cyclase
desaturase
β cyclase
α-zeacarotene
β-zeacarotene
lycopene
δ-carotene
γ-carotene
ε-carotene
α-carotene
β-carotene
hydroxyiase
α-cryptoxanthin
zeinoxanthin
β-cryptoxanthin
lutein
zeaxanthin
R =

FIG. 2

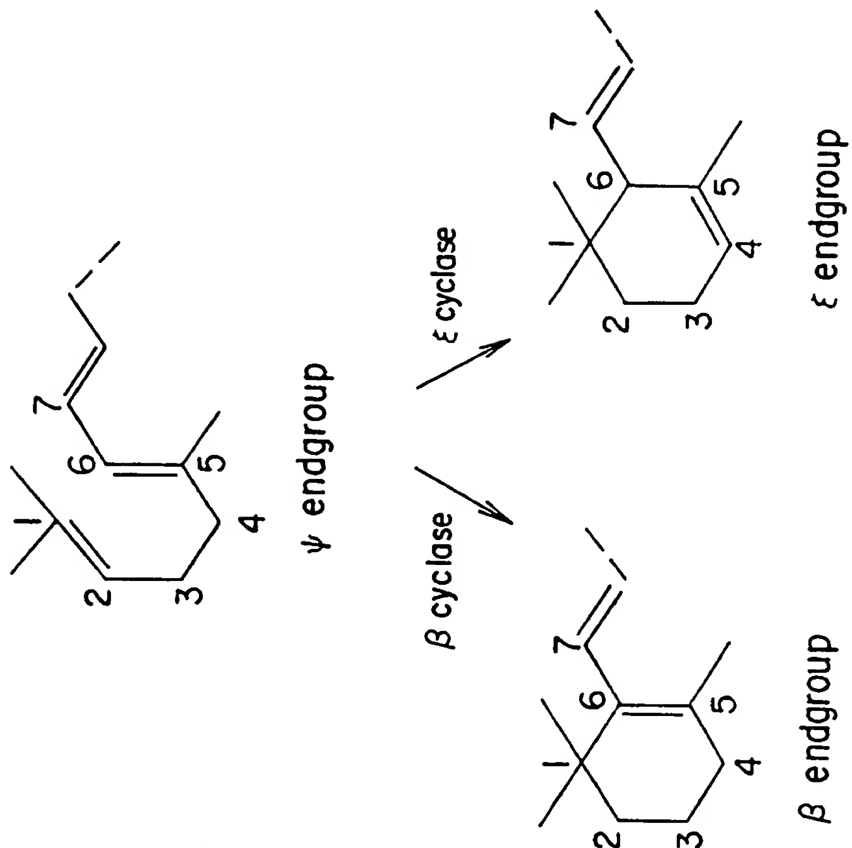


FIG. 3

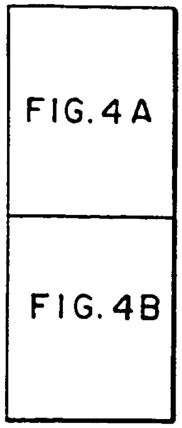


FIG. 4

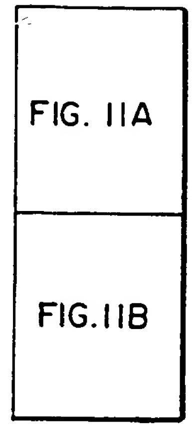


FIG. 11

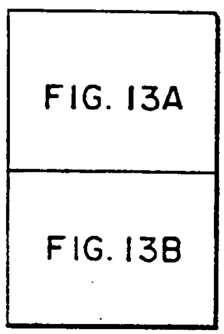


FIG. 13

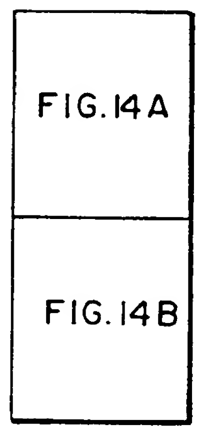


FIG. 14

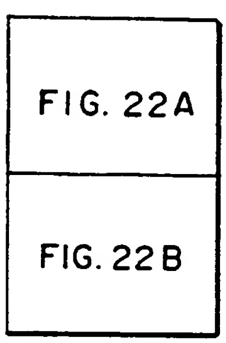


FIG. 22

FIG. 4A

Arabidopsis thaliana epsilon cyclase:

```
     acaaaaggaaataattag attcctctttctgcttgctataccttgaca  48
gaacaacataacaatggtgtaagtcttctc gctgtattcgaaattatttggaggaggaac  108
atggagtgtgttggggctaggaatttcgca gcaatggcggtttcaacatttccgtcatgg  168
1    M  E  C  V  G  A  R  N  F  A   A  M  A  V  S  T  F  P  S  W
agttgtcgaaggaaatttccagtggctaag agatacagctataggaatattcgcttcggt  228
21   S  C  R  R  K  F  P  V  V  K   R  Y  S  Y  R  N  I  R  F  G
ttgtgtagtgtcagagctagcggcggcgga agttccggtagtgagagttgtgtagcggtg  288
41   L  C  S  V  R  A  S  G  G  G   S  S  G  S  K  S  C  V  A  V
agagaagatttcgctgacgaagaagatttt gcgaaagctggcggttctgagattctattt  348
61   R  S  D  F  A  D  E  E  D  F   V  E  A  G  G  S  R  I  L  F
gttcaaatgcagcagaacaaagatatggat gaacagtctaagcttgttgataagttgcct  408
81   V  Q  M  Q  Q  M  K  D  M  D   S  Q  S  K  L  V  D  K  L  P
cctatatcaactggtgatggtgctttggat catgtggttactggctgtggtcctgctggt  468
101  P  I  S  I  G  D  G  A  L  D   K  V  V  I  G  C  G  P  A  G
ttagccttggctgcagaatcagctaagctt ggattaaaagttggactcattggtccagat  528
121  L  A  L  A  A  K  S  A  K  L   G  L  K  V  G  L  I  G  P  D
cttccttttactaacaattacggtgtttgg gaagatgaattcaatgatcttgggctgcaa  588
141  L  P  F  T  M  M  Y  G  V  M   K  D  K  F  N  D  L  G  L  G
aaatgtattgagcatgtttggagagagact attgcgcacctggatgatgacaagcctatt  648
161  K  C  I  K  K  V  W  R  S  T   I  V  Y  L  D  D  D  K  P  I
accattggccgtgcttatggaagagttagt cgacgtttgctccatgaggagcttttgagg  708
181  T  I  G  R  A  Y  G  R  V  S   R  R  L  L  X  E  E  L  L  R
aggtgtgtcgagtcaggtgtctcgtacctt agctcgaaagttgacagcataacagaagct  768
201  R  C  V  K  S  G  V  S  Y  L   S  S  K  V  D  S  I  T  E  A
tgtgatggccttagacttgttgcttgtgac gacaataacgtcattccctgcaggcttgcc  828
221  S  D  G  L  X  L  V  A  C  D   D  M  M  V  I  P  C  X  L  A
actgttgcttctggagcagcttcgggaaag ctcttgcaatacgaagttggtggacctaga  888
241  T  V  A  S  G  A  A  S  G  K   L  L  Q  Y  X  V  G  G  P  R
gtctgtgcgcaaactgcatacggcgtggag gttgaggcggaaaatagtccatatgatcca  948
```

FIG. 4B

261 V C V Q T A Y G V X V X V X N S P Y D P

gatcaaatggttttcatggattacagagat tatactaacgagaaagttcggagcttagaa 1008
281 D Q M V P M D Y R D Y T M X X V R S L X

gctgagtatccaacgtttctgtacgccatg cctatgacaaagtcaagactcttcttcgag 1068
301 A K Y P T F L Y A M P M T K S R L F F K

gagacatgtttggcctcaaaagatgtcatg ccctttgatttgctaaaaacgaagctcatg 1128
321 K T C L A S K D V M P F D L L K T K L M

ttaagattagacacactcggaattcgaatt ctaaagacttacgaagaggagtggtcctat 1188
341 I P V G G S L P N T X Q K N L A F G A A

atcccagttggtggttccttgccaaacacc gaacaaaagaatctcgcctttggtgctgcc 1248
361 I P V G G S L P M T X Q K N L A F G A A

gctagcatggtacatcccgcaacaggctat tcagttgtgagatctttgtctgaagctcca 1308
381 A S M V M P A T G Y S V V R S L S X A P

aaacatgcatcagtcatcgcagagatacta agagaagagactaccaaacagattaacagt 1368
401 K Y A S V I A K I L R E E T T K Q I N S

aatatttcaagacaagcttaggatacttta tggccaccagaaaggaaaagacagagagca 1428
421 M I S R Q A W D T L W P P E R X R Q R A

ttctttctctttggtcttgcactcagagtt caattcgataccgaaggcattagaagcttc 1488
441 F F L F G L A L I V Q F D T X G I R S F

ttccgtactttcttccgccttccaaaatgg atgtggcaagggtttctaggatcaacatta 1548
461 F R T P F R L P K W M W Q G F L G S T L

acatcaggagatctcgttctctttgcttta tacatgttcgtcatttcaccaaacaatttg 1608
481 T S G D L V L F A L Y M P V I S P M M L

agaaaaggtctcattaatcatctcatctct gatccaaccggagcaaccatgataaaaacc 1668
501 R K G L I N W L I S D P T G A T M I K T

tatctcaaagtatgatttacttaccaactc ttaggtttgtgtatatatatgccgatttat 1728

521 Y L K V

ctgaataatcgatcaaagaatggtatgtgg gttactaggaagttggaaacaaacacgtat 1788

agaatctaaggagtgatcgaaatggagacg gaaacgaaaagaaaaaaatcagtctttgtt 1848

ccgtggctagtg 1868

FIG. 5

```
1   gctctttctc ctcctcctct accgatttcc gactccgcct cccgaaatcc
51  ttatccggat tctctccgtc tcttcgattt aaacgctttt ctgtctgtta
101 cgtcgtcgaa gaacggagac agaattctcc gattgagaac gatgagagac
151 cggagagcac gagctccaca aacgctatag acgctgagta tctggcgttg
201 cgtttggcgg agaaattgga gaggaagaaa tcggagaggt ccacttatct
251 aatcgctgct atgttgtcga gctttggtat cacttctatg gctgttatgg
301 ctgtttacta cagattctct tggcaaatgg agggaggtga gatctcaatg
351 ttggaaatgt ttggtacatt tgctctctct gttggtgctg ctgttggtat
401 ggaattctgg gcaagatggg ctcatagagc tctgtggcac gcttctctat
451 ggaatatgca tgagtcacat cacaaaccaa gagaaggacc gtttgagcta
501 aacgatgttt ttgctatagt gaacgctggt ccagcgattg gtctcctctc
551 ttatggattc ttcaataaag gactcgttcc tggtctctgc tttggcgccg
601 ggttaggcat aacggtgttt ggaatcgcct acatgtttgt ccacgatggt
651 ctcgtgcaca agcgtttccc tgtaggtccc atcgccgacg tcccttacct
701 ccgaaaggtc gccgccgctc accagctaca tcacacagac aagttcaatg
751 gtgtaccata tggactgttt cttggaccca aggaattgga agaagttgga
801 ggaaatgaag agttagataa ggagattagt cggagaatca aatcatacaa
851 aaaggcctcg ggctccgggt cgagttcgag ttcttgactt taaacaagtt
901 ttaaatccca aattcttttt ttgtcttctg tcattatgat catcttaaga
951 cggtct
```

FIG. 6

```
                                                                                                64
A.thal.                        SFSS SSTDFRLRLP KSLSGFSPSL RFKRFSVCYV VEERRQNSPI ENDERPESTS STNAIDAEYL

                                                                                               144
A.thal.    ALRLAEKLER KKSERSTYLI AAMLSSFGIT SMAVMAVYYR FSWQMEGGEI SMLEMFGTFA LSVGAAVGME FWARWAHRAL
Alical.    .......... .......... .......... .......... .......... .....MTQFL IVVATVLVME LTAYSVHRWI
A.aurant.  .......... .......... .......... .......... .......... .....MTNFL IVVATVLVME LTAYSVHRWI
E.herb.    .......... .......... .......... .......... .......... ....ML.NSL IVILSVIAME GIAAFTHRYI
E.ured.    .......... .......... .......... .......... .......... ..MLWIWNAL IVIVTVIGME VIAALAHKYI
Consensus  ---------- ---------- ---------- ---------- ---------- --------f- --v-----ME --A---Hr--

                      Predicted TM helix                     Predicted TM helix

                                                                                               224
A.thal.    WHASL.WNMH ESHHKPREGP FELNDVFAIV NAGPAIGLLS YGFFNKGLVP GLCFGAGLGI TVFGIAYMFV HDGLVHKRFP
Alical.    MHGPLGWGWH KSHHEEHDHA LEKNDLYGVV FAVLATILFT VGAYWWPVLW WI....ALGM TVYGLIYFIL HDGLVHQRWP
A.aurant.  MHGPLGWGWH KSHHEEHDHA LEKNDLYGLV FAVIATVLFT VGWIWAPVLW WI....ALGM TVYGLIYFVL HDGLVHQRWP
E.herb.    MHG.WGWRWH ESHHTPRKGV FKLNDLFAVV FAGVAIALIA VGTAGVWPLQ WI....GCGM TVYGLLYFLV HDGLVHQRWP
E.ured.    MHG.WGWGWH LSHHEPRKGA FEVNDLYAVV FAALSILLIY LGSTGMWPLQ WI....GAGM TAYGLLYFMV HDGLVHQRWP
Consensus  -H--l-W--H -SHH-pr-g- fE-ND--a-V -A--ai-L-- -G-------- ------glG- Tv-G--Y--v HDGLVH-R-P

                            Predicted TM helix          Predicted TM helix

                                                                                          301
A.thal.    VGPIADVPYL RKVAAAHQLH HT..DKFNGV PYGLFLGPKE LEEVGGNEEL DKEISRRIKS YKKASGSGSS SSS*...
Alical.    FRYIPRRGYF RRLYQAHRLH HAVEGRDHCV SFGFIYAPP. VDKLKQDLKR SGVLRPQDER PS*....... .......
A.aurant.  FRYIPRKGYA RRLYQAHRLH HAVEGRDHCV SFGFIYAPP. VDKLKQDLKM SGVLRAEAQE RT*....... .......
E.herb.    FHWIPRRGYL KRLYVAHRLH HAVRGREGCV SFGFIYARK. PADLQAILRE RHGRPPKRDA AKDRPDAASP SSSSPE*
E.ured.    FRYIPRKGYL KRLYMAHRMH HAVRGKEGCV SFGFLYAPP. LSKLQATLRE RHG..ARAGA ARDAQGGEDE PASGK*.
Consensus  ---I----Yl r----AH-lH H--------V --G----p-- ---------- ---------- ---------- --s----
```

FIG. 7

```
  1 ccacgggtcc gcctccccgt ttttttccga tccgatctcc ggtgccgagg
 51 actcagctgt ttgttcgcgc tttctcagcc gtcaccatga ccgattctaa
101 cgatgctgga atggatgctg ttcagagacg actcatgttt gaagacgaat
151 gcattctcgt tgatgaaaat aatcgtgtgg tgggacatga cactaagtat
201 aactgtcatc tgatggaaaa gattgaagct gagaatttac ttcacagagc
251 tttcagtgtg tttttattca actccaagta tgagttgctt ctccagcaac
301 ggtcaaaaac aaaggttact ttcccacttg tgtggacaaa cacttgttgc
351 agccatcctc tttaccgtga atccgagctt attgaagaga atgtgcttgg
401 tgtaagaaat gccgcacaaa ggaagctttt cgatgagctc ggtattgtag
451 cagaagatgt accagtcgat gagttcactc ccttgggacg catgctttac
501 aaggcacctt ctgatgggaa atggggagag cacgaagttg actatctact
551 cttcatcgtg cgggatgtga agcttcaacc aaacccagat gaagtggctg
601 agatcaagta cgtgagcagg gaagagctta aggagctggt gaagaaagca
651 gatgctggcg atgaagctgt gaaactatct ccatggttca gattggtggt
701 ggataatttc ttgatgaagt ggtgggatca tgttgagaaa ggaactatca
751 ctgaagctgc agacatgaaa accattcaca agctctgaac tttccataag
801 ttttggatct tccccttccc ataataaaat taagagatga gacttttatt
851 gattacagac aaaactggca acaaaatcta ttcctaggat tttttttgc
901 tttttattta cttttgattc atctctagtt tagttttcat cttaaaaaa
951 aaaa
```

FIG. 8

```
1    caccaatgtc tgtttcttct ttatttaatc tcccattgat tcgcctcaga
51   tctctcgctc tttcgtcttc tttttcttct ttccGATTTG CCCATCGTCC
101  TCTGTCATCG ATTTCACCGA GAAAGTTACC GAATTTTCGT GCTTTCTCTG
151  GTACCGCTAT GACAGATACT AAAGATGCTG GTATGGATGC TGTTCAGAGA
201  CGTCTCATGT TTGAGGATGA ATGCATTCTT GTTGATGAAA CTGATCGTGT
251  TGTGGGGCAT GTCAGCAAGT ATAATTGTCA TCTGATGGAA AATATTGAAG
301  CCAAGAATTT GCTGCACAGG GCTTTTAGTG TATTTTTATT CAACTCGAAG
351  TATGAGTTGC TTCTCCAGCA AAGGTCAAAC ACAAAGGTTA CGTTCCCTCT
401  AGTGTGGACT AACACTTGTT GCAGCCATCC TCTTTACCGT GAATCAGAGC
451  TTATCCAGGA CAATGCACTA GGTGTGAGGA ATGCTGCACA AAGAAAGCTT
501  CTCGATGAGC TTGGTATTGT AGCTGAAGAT GTACCAGTCG ATGAGTTCAC
551  TCCCTTGGGA CGTATGCTGT ACAAGGCTCC TTCTGATGGC AAATGGGGAG
601  AGCATGAACT TGATTACTTG CTCTTCATCG TGCGAGACGT GAAGGTTCAA
651  CCAAACCCAG ATGAAGTAGC TGAGATCAAG TATGTGAGCC GGGAAGAGCT
701  GAAGGAGCTG GTGAAGAAAG CAGATGCAGG TGAGGAAGGT TTGAAACTGT
751  CACCATGGTT CAGATTGGTG GTGGACAATT TCTTGATGAA GTGGTGGGAT
801  CATGTTGAGA AAGGAACTTT GGTTGAAGCT ATAGACATGA AAACCATCCA
851  CAAACTCTGA ACATCTTTTT TTAAAGTTTT TAAATCAATC AACTTTCTCT
901  TCATCATTTT TATCTTTTCG ATGATAATAA TTTGGGATAT GTGAGACACT
951  TACAAAACTT CCAAGCACCT CAGGCAATAA TAAAGTTTGC GGCCGC
```

FIG. 9

```
   1 CTCGGTAGCT GGCCACAATC GCTATTTGGA ACCTGGCCCG GCGGCAGTCC
  51 GATGCCGCGA TGCTTCGTTC GTTGCTCAGA GGCCTCACGC ATATCCCCCG
 101 CGTGAACTCC GCCCAGCAGC CCAGCTGTGC ACACGCGCGA CTCCAGTTTA
 151 AGCTCAGGAG CATGCAGATG ACGCTCATGC AGCCCAGCAT CTCAGCCAAT
 201 CTGTCGCGCG CCGAGGACCG CACAGACCAC ATGAGGGGTG CAAGCACCTG
 251 GGCAGGCGGG CAGTCGCAGG ATGAGCTGAT GCTGAAGGAC GAGTGCATCT
 301 TGGTGGATGT TGAGGACAAC ATCACAGGCC ATGCCAGCAA GCTGGAGTGT
 351 CACAAGTTCC TACCACATCA GCCTGCAGGC CTGCTGCACC GGGCCTTCTC
 401 TGTGTTCCTG TTTGACGATC AGGGGCGACT GCTGCTGCAA CAGCGTGCAC
 451 GCTCAAAAAT CACCTTCCCA AGTGTGTGGA CGAACACCTG CTGCAGCCAC
 501 CCTTTACATG GGCAGACCCC AGATGAGGTG GACCAACTAA GCCAGGTGGC
 551 CGACGGAACA GTACCTGGCG CAAAGGCTGC TGCCATCCGC AAGTTGGAGC
 601 ACGAGCTGGG GATACCAGCG CACCAGCTGC CGGCAAGCGC GTTTCGCTTC
 651 CTCACGCGTT TGCACTACTG TGCCGCGGAC GTGCAGCCAG CTGCGACACA
 701 ATCAGCGCTC TGGGGCGAGC ACGAAATGGA CTACATCTTG TTCATCCGGG
 751 CCAACGTCAC CTTGGCGCCC AACCCTGACG AGGTGGACGA AGTCAGGTAC
 801 GTGACGCAAG AGGAGCTGCG GCAGATGATG CAGCCGGACA ACGGGCTGCA
 851 ATGGTCGCCG TGGTTTCGCA TCATCGCCGC GCGCTTCCTT GAGCGTTGGT
 901 GGGCTGACCT GGACGCGGCC CTAAACACTG ACAAACACGA GGATTGGGGA
 951 ACGGTGCATC ACATCAACGA AGCGTGAAAG CAGAAGCTGC AGGATGTGAA
1001 GACACGTCAT GGGGTGGAAT TGCGTACTTG GCAGCTTCGT ATCTCCTTTT
1051 TCTGAGACTG AACCTGCAGT CAGGTCCCAC AAGGTCAGGT AAAATGGCTC
1101 GATAAAATGT ACCGTCACTT TTTGTCGCGT ATACTGAACT CCAAGAGGTC
1151 AAAAAAAAAA AAAAA
```

FIG. 10

1	CTCGGTAGCT	GGCCACAATC	GCTATTTGGA	ACCTGGCCCG	GCGGCAGTCC
51	GATGCCGCGA	TGCTTCGTTC	GTTGCTCAGA	GGCCTCACGC	ATATCCCGCG
101	CGTGAACTCC	GCCCAGCAGC	CCAGCTGTGC	ACACGCGCGA	CTCCAGTTTA
151	AGCTCAGGAG	CATGCAGCTG	CTTTCCGAGG	ACCGCACAGA	CCACATGAGG
201	GGTGCAAGCA	CCTGGGCAGG	CGGGCAGTCG	CAGGATGAGC	TGATGCTGAA
251	GGACGAGTGC	ATCTTGGTAG	ATGTTGAGGA	CAACATCACA	GGCCATGCCA
301	GCAAGCTGGA	GTGTCACAAG	TTCCTACCAC	ATCAGCCTGC	AGGCCTGCTG
351	CACCGGGCCT	TCTCTGTGTT	CCTGTTTGAC	GATCAGGGGC	GACTGCTGCT
401	GCAACAGCGT	GCACGCTCAA	AAATCACCTT	CCCAAGTGTG	TGGACGAACA
451	CCTGCTGCAG	CCACCCTTTA	CATGGGCAGA	CCCCAGATGA	GGTGGACCAA
501	CTAAGCCAGG	TGGCCGACGG	AACAGTACCT	GGCGCAAAGG	CTGCTGCCAT
551	CCGCAAGTTG	GAGCACGAGC	TGGGGATACC	AGCGCACCAG	CTGCCGGCAA
601	GCGCGTTTCG	CTTCCTCACG	CGTTTGCACT	ACTGTGCCGC	GGACGTGCAG
651	CCAGCTGCGA	CACAATCAGC	GCTCTGGGGC	GAGCACGAAA	TGGACTACAT
701	CTTGTTCATC	CGGGCCAACG	TCACCTTGGC	GCCCAACCCT	GACGAGGTGG
751	ACGAAGTCAG	GTACGTGACG	CAAGAGGAGC	TGCGGCAGAT	GATGCAGCCG
801	GACAACGGGC	TTCAATGGTC	GCCGTGGTTT	CGCATCATCG	CCGCGCGCTT
851	CCTTGAGCGT	TGGTGGGCTG	ACCTGGACGC	GGCCCTAAAC	ACTGACAAAC
901	ACGAGGATTG	GGGAACGGTG	CATCACATCA	ACGAAGCGTG	AAGGCAGAAG
951	CTGCAGGATG	TGAAGACACG	TCATGGGGTG	GAATTGCGTA	CTTGGCAGCT
1001	TCGTATCTCC	TTTTTCTGAG	ACTGAACCTG	CAGAGCTAGA	GTCAATGGTG
1051	CATCATATTC	ATCGTCTCTC	TTTTGTTTTA	GACTAATCTG	TAGCTAGAGT
1101	CACTGATGAA	TCCTTTACAA	CTTTCAAAAA	AAAAA	

FIG. 11A

	1				50
HPO4	MLRSLLRGLT	HIPRVNSAQQ	PSCAHARLQF	KLRSMQMTLM	QPSISANLSR
HPO5	MLRSLLRGLT	HIPRVNSAQQ	PSCAHARLQF	KLRSMQLL..	....
ATDP7	MSVSSLFNLP	.LIRLRSLA.	LSSSFSSFRF	AHRPLSSIS.	PRKLPNFRAF
C.brew.	MS.SSMLNFT	.ASRIVSLPL	LSSPPSRVHL	PLCFFSPISL	TQRFSAKLTF
ATOP5	....	.TGPPPRFFP	IRSPVPRTQL	FVRAFSAV..	....
S.cerev.	..MTADNNSM	PHGAVSSYAK	LVQNQTPEDI	LEEFPEIIPL	QQRPN...TR

51				100
AEDRTDHMRG	ASTWAGGQSQ	DELMLKDECI	LVDVEDNITG	HASKLECHKF
SEDRTDHMRG	ASTWAGGQSQ	DELMLKDECI	LVDVEDNITG	HASKLECHKF
S..GTA.MTD	TKDAGMDAVQ	RRLMFEDECI	LVDETDRVVG	HVSKYNCHLM
SSQATT.MGE	VVDAGMDAVQ	RRLMFEDECI	LVDENDKVVG	HESKYNCHLM
.....T.MTD	SNDAGMDAVQ	RRLMFEDECI	LVDENNRVVG	HDTKYNCHLM
SSETSNDESG	ETCFSGHDEE	QIKLMNENCI	VLDWDDNAIG	AGTKKVCHLM

101				150
LPHQPAGLLH	RAFSVFLFDD	QGRLLLQQRA	RSKITFPSVW	TNTCCSHPLH
LPHQPAGLLH	RAFSVFLFDD	QGRLLLQQRA	RSKITFPSVW	TNTCCSHPLH
ENIEAKNLLH	RAFSVFLFNS	KYELLLQQRS	NTKVTFPLVW	TNTCCSHPLY
ENIESENLLH	RAFSVFLFNS	KYELLLQQRS	ATKVTFPLVW	TNTCCSHPLY
EKIEAENLLH	RAFSVFLFNS	KYELLLQQRS	KTKVTFPLVW	TNTCCSHPLY
ENIE.KGLLH	RAFSVFIFNE	QGELLLQQRA	TEKITFPDLW	TNTCCSHPLC

151				200
GQTPDEVDQL	SQVADGTVPG	AKAAAIRKLE	HELGIPAHQL	PA.SAFRFLT
GQTPDEVDQL	SQVADGTVPG	AKAAAIRKLE	HELGIPAHQL	PA.SAFRFLT
RE........	SELIQDNALG	VRNAAQRKLL	DELGIVAEDV	PV.DEFTPLG
RE........	SELIDENCLG	VRNAAQRKLL	DELGIPAEDL	PV.DQFIPLS
RE........	SELIEENVLG	VRNAAQRKLF	DELGIVAEDV	PV.DEFTPLG
ID...DELGL	KGKLDDKIKG	AITAAVRKLD	HELGIPEDET	KTRGKFHFLN

201				250
RLHYCAADVQ	PAATQSALWG	EHEMDYILFI	....RANVTL	APNPDEVDEV
RLHYCAADVQ	PAATQSALWG	EHEMDYILFI	....RANVTL	APNPDEVDEV
RMLY......	.KAPSDGKWG	EHELDYLLFI	....VRDVKV	QPNPDEVAEI
RILY......	.KAPSDGKWG	EHELDYLLFI	....IRDVNL	DPNPDEVAEV
RMLY......	.KAPSDGKWG	EHEVDYLLFI	....VRDVKL	QPNPDEVAEI
RIHY......	.MAPSNEPWG	EHEIDYILFY	KINAKENLTV	NPNVNEVRDF

FIG. 11B

```
251                                                    300
RYVTQEELRQ MMQ....PDN GLQWSPWFRI IAARFLERWW ADLDAALNTD
RYVTQEELRQ MMQ....PDN GLQWSPWFRI IAARFLERWW ADLDAALNTD
KYVSREELKE LVKKADAGEE GLKLSPWFRL VVDNFLMKWW DHVEKGTLVE
KYMNRDDLKE LLRKADAEEE GVKLSPWFRL VVDNFLFKWW DHVEKGSLKD
KYVSREELKE LVKKADAGDE AVKLSPWFRL VVDNFLMKWW DHVEKGTITE
KWVSPNDLKT MF.....ADP SYKFTPWFKI ICENYLFNWW EQLDDLSEVE

301
KHEDWGTVHH INEA*
KHEDWGTVHH INEA*
A.IDMKTIHK L*
A.ADMKTIHK L*
A.ADMKTIHK L*
A.ADMKTIHK L*
NDRQ...IHR ML*
```

FIG. 12

```
1   ccaaaaacaa ctcaaatctc ctccgtcgct cttactccgc catgggtgac
51  gactccggca tggatgctgt tcagcgacgt ctcatgtttg acgatgaatg
101 cattttggtg gatgagtgtg acaatgtggt gggacatgat accaaataca
151 attgtcactt gatggagaag attgaaacag gtaaaatgct gcacagagca
201 ttcagcgttt ttctattcaa ttcaaaatac gagttacttc ttcagcaacg
251 gtctgcaacc aaggtgacat ttcctttagt atggaccaac acctgttgca
301 gccatccact ctacagagaa tccgagcttg ttcccgaaac gcctgagaga
351 atgctgcaca gaggaxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
401 xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
451 xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
501 xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
551 xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
601 xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
651 xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx tcatgtgcaa aagggtacac
701 tcactgaatg caatttgata tgaaaaccat acacaagctg atatagaaac
751 acaccctcaa ccgaaaagca agcctaataa ttcgggttgg gtcgggtcta
801 ccatcaattg ttttttttctt ttaacaactt ttaatctcta tttgagcatg
851 ttgattcttg tcttttgtgt gtaagatttt gggtttcgtt tcagttgtaa
901 taatgaacca ttgatggttt gcaatttcaa gttcctatcg acatgtagtg
951 atctaaaaaa
```

FIG. 13A

```
              1                                                                  70
Plant beta    .......... ...MDTLLkT PN-LaFl-p- -HG.....F- vk.-S-f-s- k---fG--K- cs--g---vc
A.t.epsilon   MECVGARNFA AMAVSTFPSW SCRRKFPVVK RYSYRNIRFG LCSVRASGGG SSGSESCVAV REDFADEXDF
Consensus     ---------- -----T---- -----F---- --------F- ---------- ---------- -E--------

                         Cyanobacterial enzyme begins
              71                                                                 140
Plant beta    Vk--SsALLa LVPETKKKNL DFELPmYDp. ...S.Kg-VV DLAvVGGGPA GLAVAQQVSE AGLSVcSIDp
A.t.epsilon   VKAGGSEIL. FVQMQQNKDM DEQSKLVDKL PPISIGDGAL DHVVIGCGPA GLALAAESAK LGLKVGLIGP
Consensus     VK---S--L- -V-------- D------D-- ---S------ D--V-G-GPA GLA-A----- -GL-V--I-P

              Possible subunit interaction domain        Dinucleotide-binding signature

              141                                                                210
Plant beta    .-PKLIWPNN YGVWVDEFEA MDLLDCLDaT WSGa-VYiDd -t-KDL-RPY GRVNRKQLKS KMmQKCI-NG
A.t.epsilon   DLP...FTNN YGVWEDEFND LGLQKCIEHV WRETIVYLDD DKPITIGRAY GRVSRRLLHE ELLRRCVESG
Consensus     --P-----NN YGVW-DEF-- --L--C---- W----VY-DD -------R-Y GRV-R--L-- -----C---G

                   Conserved region #1

              211                                                                280
Plant beta    VKFHgaKVik ViHE.E-kSm liCnDG-tIQ AtVVLDATGF SR-.LVQYDK PYnPGY.QVA YGILAEVeeH
A.t.epsilon   VSYLSSKVDS ITKASDGLRL VACDDNNVIP CRLATVASGA ASGKLLQYEV GGPRVCVQTA YGVEVEVENS
Consensus     V-----KV-- ---------- --C-D---I- ------A-G- ----L-QY-- -------Q-A YG---gv---
```

```
                281                                                                    350
Plant beta      PFD--KMVfM DWRDsHL-NN -eLKERNs-i PTFLYAMPFS SNrIFLEETS LVARPGLmd DIQERMvARL
A.t.epsilon     PYDPDQMVFM DYRDY..TNE .KVRSLEAEY PTFLYAMPMT KSRLFFEXTC LASKDVMPFD LLKTKLMLRL
Consensus       P-D---MVFM D-RD----N- ---------- PTFLYAMP-- --R-F-EXT- L--------D --------RL
                  Conserved region #2                  Conserved region #3

                351                                                                    420
Plant beta      -HLGIkVKsI EEDEhCvIPM GGpLPVlPQR VVGiGGTAGm VHPSTGYMVA RTLAAAPvVA NAIi-YLgSe
A.t.epsilon     DTLGTRILKT YEEEWSVIPV GGSLPNTEQK NLAFGAAASM VHPATGYSVV RSLSEAPKYA SVIAEILREE
Consensus       --LGI----- -E-E---IP- GG-LP---Q- ----G--A-M VHP-TGY-V- R-L--AP--A --I---L--E
                                                      Conserved region #4   Predicted TM helix

                421                                                         480
Plant beta      -s-s..G-eL SaeVWkDLWP IERRRQREFF CFGMDILLKL DLpATRRFFD AFFDLaPrYW
A.t.epsilon     TTKQINSN.I SRQAWDTLWP PERKRQRAFF LFGLALIVQF DTEGIRSFFR TFFRLPKWMW
Consensus       ---------- S---W--LWP -ER-RQR-FF -FG------- D----R-FF- -FF-L----W
                             Conserved region #5

                481                                                533
Plant beta      HGFLSSRLfL PELivFGLSL FShASNTSR- EIMTK.GT-P Lv-MINNLlQ D--
A.t.epsilon     QGFLGSTLTS GDLVLFALYM FVISPNNLRK GLINHLISDP TGATMIKTYL KV.
Consensus       -GFL-S-L-- --L--F-L-- F----N--R- ---------- ---------- ---
                   Predicted TM helix
```

FIG. 13B

FIG. 14A

Adonis palaestina ε-cyclase cDNA #5 Length: 1898

```
   1 aaaggagtgt tctattaatg ttactgtcgc attcttgcaa cacttatatt
  51 caaactccat tttcttcttt tctcttcaaa acaacaaact aatgtgagca
 101 gagtatctgg ctatggaact acttggtgtt cgcaacctca tctcttcttg
 151 ccctgtgtgg acttttggaa caagaaacct tagtagttca aaactagctt
 201 ataacataca tcgatatggt tcttcttgta gagtagattt tcaagtgaga
 251 gctgatggtg gaagcgggag tagaagttct gttgcttata aagagggttt
 301 tgtggatgaa gaggatttta tcaaagctgg tggttctgag cttttgtttg
 351 tccaaatgca gcaaacaaag tctatggaga aacaggccaa gctcgccgat
 401 aagttgccac caataccttt tggagaatcc gtgatggact tggttgtaat
 451 aggttgtgga cctgctggtc tttcactggc tgcagaagct gctaagctag
 501 ggttgaaagt tggccttatt ggtcctgatc ttccttttac aaataattat
 551 ggtgtgtggg aagacgagtt caaagatctt ggacttgaac gttgtatcga
 601 gcatgcttgg aaggacacca tcgtatatct tgataatgat gctcctgtcc
 651 ttattggtcg tgcatatgga cgagttagtc gacatttgct acatgaggag
 701 ttgctgaaaa ggtgtgtgga gtcaggtgta tcatatctgg attctaaagt
 751 ggaaaggatc actgaagctg gtgatggcca tagccttgta gtttgtgaaa
 801 atgagatctt tatcccttgc aggcttgcta ctgttgcatc tggagcagct
 851 tcagggaaac ttttggagta tgaagtaggt ggccctcgtg tttgtgtcca
 901 aaccgcttat ggggtggagg ttgaggtgga gaacaatcca tacgatccca
 951 acttaatggt attcatggac tacagagact atatgcaaca gaaattacag
1001 tgctcggaag aagaatatcc aacatttctC tatgtcatgc ccatgtcgcc
1051 aacaagactt ttttttgagg aaacctgttt ggcctcaaaa gatgccatgc
1101 cattcgatct actgaagaga aaactgatgt cacgattgaa gactctgggt
1151 atccaagtta caaaagttta tgaagaggaa tggtcatata ttcctgttgg
1201 tggttcttta ccaaacacag agcaaaagaa cctagcattt ggtgctgcag
1251 caagcatggt gcatccagca acaggctatt cggttgtacg gtcactgtca
1301 gaagctccaa aatatgcttc tgtaattgca aagattttga agcaagataa
1351 ctctgcgtat gtggtttctg gacaaagtag tgcagtaaac atttcaatgc
1401 aagcatggag cagtctttgg ccaaaggagc gaaaacgtca aagagcatTc
1451 tttcttttTg gattagagct tattgtgcag ctagatattg aagcaaccag
1501 aacattcttt agaaccttct tccgcttgcc aacttggatg tggtggggtt
1551 tccttgggtc ttcactatca tctttcgatc tcgtcttgtt ttccatgtac
1601 atgtttgttt tggcgccaaa cagcatgagg atgtcacttg tgagacattt
1651 gctttcagat ccttctggtg cagttatggt aagagcttac ctcgaaaggt
1701 agtctcatct attattaaac tctagtgttt caccaaataa atgaggatcc
1751 ttcgaatgtg tatatgatca tctctatgta tatcctgtac tctaatctca
1801 taaagtaaat gccgggtttg atattgttgt gtcaaaccgg ccaatgatat
1851 aaagtaaatt tattgataca aaagtagttt ttttccttaa aaaaaaa
```

FIG. 14B

Adonis palaestina ε-cyclase #5 predicted polypeptide
TRANSLATE from: 113 to: 1702 Length: 529 amino acids

```
  1  MELLGVRNLI SSCPVWTFGT RNLSSSKLAY NIHRYGSSCR VDFQVRADGG
 51  SGSRSSVAYK EGFVDEEDFI KAGGSELLFV QMQQTKSMEK QAKLADKLPP
101  IPFGESVMDL VVIGCGPAGL SLAAEAAKLG LKVGLIGPDL PFTNNYGVWE
151  DEFKDLGLER CIEHAWKDTI VYLDNDAPVL IGRAYGRVSR HLLHEELLKR
201  CVESGVSYLD SKVERITEAG DGHSLVVCEN EIFIPCRLAT VASGAASGKL
251  LEYEVGGPRV CVQTAYGVEV EVENNPYDPN LMVFMDYRDY MQQKLQCSEE
301  EYPTFLYVMP MSPTRLFFEE TCLASKDAMP FDLLKRKLMS RLKTLGIQVT
351  KVYEEEWSYI PVGGSLPNTE QKNLAFGAAA SMVHPATGYS VVRSLSEAPK
401  YASVIAKILK QDNSAYVVSG QSSAVNISMQ AWSSLWPKER KRQRAFFLFG
451  LELIVQLDIE ATRTFFRTFF RLPTWMWWGF LGSSLSSFDL VLFSMYMFVL
501  APNSMRMSLV RHLLSDPSGA VMVRAYLER*
```

FIG. 15A

DNA sequence of potato cDNA (GenBank R27545) obtained from Nicholas J. Provart

```
potato.seq  Length: 1378  August 2, 1996  13:06  Type: N  Check: 605  ..
   1  tagcggnnnn naggatgagt tcaaagatct tggtcttcaa gcctgcattg
  51  aacatgtttg gcgggatacc attgtatatc ttgatgatga tgatcctatt
 101  cttattggcc gtgcctatgg aagagttagt cgccatttac tgcacgagga
 151  gttactcaaa aggtgtgtgg aggcaggtgt tttgtatcta aactcgaaag
 201  tggataggat tgttgaggcc acaaatggcc acagtcttgt agagtgcgag
 251  ggtgatgttg tgattccctg caggtttgtg actgttgcat cgggagcagc
 301  ctcggggaaa ttcttgcagt atgagttggg aggtcctaga gtttctgttc
 351  aaacagctta tggagtggaa gttgaggtcg ataacaatcc atttgacccg
 401  agcctgatgg ttttcatgga ttatagagac tatgtcagac acgacgctca
 451  atctttagaa gctaaatatc caacatttct ctatgccatg cccatgtctc
 501  caacacgagt ctttttcgag gaaacttgtt tggcttcaaa agatgcaatg
 551  ccattcgatc tgttaaagaa aaaattgatg ttacgattga acaccctcgg
 601  tgtaagaatt aaagaaattt atgaggagga atggtcttac ataccagttg
 651  gaggatcttt gccaaataca gaacaaaaaa cacttgcatt tggtgctgct
 701  gctagcatgg ttcatccagc cacaggttat tcagtcgtca gatcactgtc
 751  tgaagctcca aaatgcgcct tcgtgcttgc aaatatatta cgacaaaatc
 801  atagcaagaa tatgcttact agttcaagta ccccgagtat ttcaactcaa
 851  gcttggaaca ctctttggcc acaagaacga aaacgacaaa gatcgttttt
 901  cctatttgga ctggctctga tattgcagct ggatattgag ggataaggt
 951  catttttccg cgcgttcttc cgtgtgccaa aatggatgtg gcagggattt
1001  cttggttcaa gtctttcttn agcagacctc atgttatttg ccttctacat
1051  gtttattatt gcaccaaatg acatgagaag aggcttaatc agacatcttt
1101  tatctgatcc tactggtgca acattgataa gaacttatct tacattttag
1151  agtaaattcc tcctacaata gttgttgaan nagaggcctc attacttcag
1201  attcataaca gaaatcgcgg tctctcgagg ccttgtatat aacattttca
1251  ctaggttaat attgcttgaa taagttgcac agtttcagtt tttgtatctg
1301  cttctttttt gtccaagatc atgtattgan ccaatttata tacattgcca
1351  gtatatataa attttataaa aaaaaaaa

poteps.pep  Length: 378   TRANSLATE from: 14  to: 1147
   1  DEFKDLGLQA CIEHVWRDTI VYLDDDDPIL IGRAYGRVSR HLLHEELLKR
  51  CVEAGVLYLN SKVDRIVEAT NGHSLVECEG DVVIPCRFVT VASGAASGKF
 101  LQYELGGPRV SVQTAYGVEV EVDNNPFDPS LMVFMDYRDY VRHDAQSLEA
 151  KYPTFLYAMP MSPTRVFFEE TCLASKDAMP FDLLKKKLML RLNTLGVRIK
 201  EIYEEEWSYI PYGGSLPNTE QKTLAFGAAA SMVHPATGYS VVRSLSEAPK
 251  CAFVLANILR QNHSKNMLTS SSTPSISTQA WNTLWPQERK RQRSFFLFGL
 301  ALILQLDIEG IRSFFRAFFR VPKWMWQGFL GSSLSXADLM LFAFYMFIIA
 351  PNDMRRGLIR HLLSDPTGAT LIRTYLTF*
```

FIG. 15B

Chimeric lettuce/potato lycopene ε-cyclase: converts lycopene to δ-carotene, the lettuce cDNA converts lycopene to ε-carotene and the potato cDNA does not produce an active enzyme

(amino acids in lower case are from lettuce and those in uppercase are from the potato cDNA; an *Ava*II site in common to the two cDNAs was used to construct the chimera)

```
  1 mecfgarnmt atmavftcpt ftdcnirhkf sllkqrrftn lsassslrqi
 51 kcsaksdrcv vdkqgisvac eedyvkaggs elffvqmqrt ksmesqskls
101 eklaqipign cildlvvigc gpaglalaae saklglnvgl igpdlpftnn
151 ygvwqdefig lglegciehs wkdtlvyldd adpirigray grvhrdllhe
201 ellrrcvesg vsylsskver iteapngysl iecegnitip crlatvasga
251 asgkfleyel gGPRVSVQTA YGVEVEVDNN PFDPSLMVFM DYRDYVRHDA
301 QSLEAKYPTF LYAMPMSPTR VFFEETCLAS KDAMPFDLLK KKLMLRLNTL
351 GVRIKEIYEE EWSYIPVGGS LPNTEQKTLA FGAAASMVHP ATGYSVVRSL
401 SEAPKCAFVL ANILRQNHSK NMLTSSSTPS ISTQAWNTLW PQERKRQRSF
451 FLFGLALILQ LDIEGIRSFF RAFFRVPKWM WQGFLGSSLS XADLMLFAFY
501 MFIIAPNDMR RGLIRHLLSD PTGATLIRTY LTF*
```

FIG. 16

```
GAP comparison of Arabidopsis ε-cyclase x potato ε-cyclase (partial)
 blosum62.cmp   Gap Weight:       12      Average Match:  2.912
              Length Weight:       4    Average Mismatch: -2.003
                    Quality:    1485             Length:    529
                      Ratio:   3.929               Gaps:      1
       Percent Similarity: 79.893   Percent Identity: 76.139
Match display thresholds for the alignment(s):
                | = IDENTITY    : = 2    . = 1

                   .         .         .         .         .
 151 EDEFNDLGLQKCIEHVWRETIVYLDDDKPITIGRAYGRVSRRLLHEELLR 200
      ||| ||||| |||||||:|||||||| || |||||||||| |||||||:
   1 .DEFKDLGLQACIEHVWRDTIVYLDDDDPILIGRAYGRVSRHLLHEELLK 49
                   .         .         .         .         .
 201 RCVESGVSYLSSKVDSITEASDGLRLVACDDNNVIPCRLATVASGAASGK 250
     ||||.|| ||.|||| | ||..|  || |: . |||||  ||||||||||
  50 RCVEAGVLYLNSKVDRIVEATNGHSLVECEGDVVIPCRFVTVASGAASGK 99
                   .         .         .         .         .
 251 LLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVFMDYRDYTNEKVRSLE 300
      ||||.|||||  |||||||||||:|.|:||  ||  ||||||      .|||
 100 FLQYELGGPRVSVQTAYGVEVEVDNNPFDPSLMVEMDYRDYVRHDAQSLE 149
                   .         .         .         .         .
 301 AEYPTFLYAMPMTKSRLFFEETCLASKDVMPFDLLKTKLMLRLDTLGIRI 350
     |.||||||||||. .|.||||||||||| ||||||| ||||||.|||:||
 150 AKYPTFLYAMPMSPTRVFFEETCLASKDAMPFDLLKKKLMLRLNTLGVRI 199
                   .         .         .         .         .
 351 LKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAP 400
       .|||||||||||||||||||| ||||||||||||||||||||||||||
 200 KEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAP 249
                   .         .         .         .         .
 401 KYASVIAEILREETTKQI.....NSNISRQAWDTLWPPERKRQRAFFLFG 445
     | | |:| |||:  .| .     .|| |||.|||| ||||||.|||||
 250 KCAFVLANILRQNHSKNMLTSSSTPSISTQAWNTLWPQERKRQRSFFLFG 299
                   .         .         .         .         .
 446 LALIVQFDTEGIRSFFRTFFRLPKWMWQGFLGSTLTSGDLVLFALYMFVI 495
     ||||.| | |||||||| |||.|||||||||||.|.  ||.||| |||:|
 300 LALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSXADLMLFAFYMFII 349
                   .         .
 496 SPNNLRKGLINHLISDPTGATMIKTYLKV 524
     .||.:|:||| ||:|||||||:|:|||
 350 APNDMRRGLIRHLLSDPTGATLIRTYLTF 378
```

FIG. 17A

Adonis palaestina Ipi1

```
   1 attcatcttc agcagcgctg tcgtactctt tctatatctt cttccatcac
  51 taacagtagt cgccgacggt tgaatcggct attcgcctca acgtcaacta
 101 tgggtgaagt cactgatgct ggaatggatg ctgttcagaa gcggctcatg
 151 ttcgacgacg aatgtatttt ggtggatgag aatgacaagg tcgtcgggca
 201 tgattccaaa tacaactgtc atttgatgga aaagatagag gcagaaaatt
 251 tgcttcacag agccttcagt gttttcttgt tcaactcaaa atatgaattg
 301 cttcttcagc aacgatccgc cacaaaggta acattcccgc tcgtatggac
 351 aaacacatgt tgcagtcatc ctctctttcg tgattccgag ctcatagaag
 401 aaaattatct cggtgtacga aacgctgcac aaagaaagct tttagacgag
 451 ctaggcattc cagctgaaga tgtcccagtt gatgaattta ctcctcttgg
 501 tcgcattctt tacaaagctc catctgacgg caaatgggga gagcacgaat
 551 tggactatct cctatttatt gtccgagatg tgaaatacga tccaaaccca
 601 gatgaagttg ctgatgctaa gtatgttaat cgcgaggagt tgagagagat
 651 actgagaaaa gctgatgctg gtgaagaggg actcaagttg tctccttggt
 701 ttagattggt tgttgataac tttttgttca agtggtggga tcatgtagag
 751 cagggtacga ttaaggaagt tgctgacatg aaaactatcc acaagttgac
 801 ttaagaggac ttctctcctc tgttctacta tttgtttttt gctacaataa
 851 gtgggtggtg ataagcagtt tttctgtttt ctttaattta tggcttttga
 901 atttgcctcg atgttgaact tgtaacatat ttagacaaat atgagacctt
 951 gtaagttgaa tttgaggctg aatttatatt tttgggaaca taataatgtt
1001 aa
```

FIG. 17B

Adonis palaestina Ipi2

```
   1 ttttaaagct ctttcgctcc accaccatca aagccagcca aatttctctg
  51 tacaaaagtt aaaaacaccg ctttgggctt tggccccctcc atatcggaat
 101 ccttgtttac gatacgcatc taaaccagta attctcggtt ttaatttgtt
 151 tcctaaatta ggccccctttc cggaatcccg agaattatgt cgtcgatcag
 201 gattaatcct ttatatagta tcttctccac caccactaaa acattatcag
 251 cttcgtgttc ttctcccgct gttcatcttc agcagcgttg tcgtactctt
 301 tctatttctt cttccatcac taacagtcct cgccgagggt tgaatcggct
 351 gttcgcctca acgtcgacta tgggtgaagt cgctgatgct ggtatggatg
 401 ccgtccagaa gcggcttatg ttcgacgatg aatgtatttt ggtggatgag
 451 aatgacaagg tcgtcggaca tgattccaaa tacaactgtc atttgatgga
 501 aaagatagag gcagaaaact tgcttcacag agccttcagt gttttcttat
 551 tcaactcaaa atacgagttg cttcttcagc aacgatctgc aacgaaggta
 601 acattcccgc tcgtatggac aaacacctgt tgcagccatc ccctcttccg
 651 tgattccgaa ctcatagaag aaaattttct cggggtacga aacgctgcac
 701 aaaggaagct tttagacgag ctaggcattc cagctgaaga cgtaccagtt
 751 gatgaattca ctcctcttgg tcgcattctt tacaaagctc catctgacgg
 801 aaaatgggga gagcacgaac tggactatct tctgtttatt gtccgagatg
 851 tgaaatacga tccaaaccca gatgaagttg ctgacgctaa gtacgttaat
 901 cgcgaggagt tgaaagagat actgagaaaa gctgatgcag gtgaagaggg
 951 aataaagttg tctccttggt ttagattggt tgtggataac tttttgttca
1001 agtggtggga tcatgtagag gaggggaaga ttaaggacgt cgccgacatg
1051 aaaactatcc acaagttgac ttaagagaaa gtctcttaag ttctactatt
1101 tggtttttgc ttcaataagt ggatggtgat gagcagtttt tatgcttcct
1151 ttaattttgg cttttcaatt tgctttatgt gttgaacttg taacatattt
1201 agtcaaatat gagaccttgt gagttgaatt tgaggttata tttatagttt
1251 tgggaacata aaaaaaaaaa
```

FIG. 18A

Haematococcus pluvialis Ipi1

```
   1  ctcggtagct ggccacaatc gctatttgga acctggcccg gcggcagtcc
  51  gatgccgcga tgcttcgttc gttgctcaga ggcctcacgc atatcccccg
 101  cgtgaactcc gcccagcagc ccagctgtgc acacgcgcga ctccagttta
 151  agctcaggag catgcagatg acgctcatgc agcccagcat ctcagccaat
 201  ctgtcgcgcg ccgaggaccg cacagaccac atgaggggtg caagcacctg
 251  ggcaggcggg cagtcgcagg atgagctgat gctgaaggac gagtgcatct
 301  tggtggatgt tgaggacaac atcacaggcc atgccagcaa gctggagtgt
 351  cacaagttcc taccacatca gcctgcaggc ctgctgcacc gggccttctc
 401  tgtgttcctg tttgacgatc aggggcgact gctgctgcaa cagcgtgcac
 451  gctcaaaaat caccttccca agtgtgtgga cgaacacctg ctgcagccac
 501  cctttacatg ggcagacccc agatgaggtg gaccaactaa gccaggtggc
 551  cgacggaaca gtacctggcg caaaggctgc tgccatccgc aagttggagc
 601  acgagctggg gataccagcg caccagctgc cggcaagcgc gtttcgcttc
 651  ctcacgcgtt tgcactactg tgccgcggac gtgcagccag ctgcgacaca
 701  atcagcgctc tggggcgagc acgaaatgga ctacatcttg ttcatccggg
 751  ccaacgtcac cttggcgccc aaccctgacg aggtggacga agtcaggtac
 801  gtgacgcaag aggagctgcg gcagatgatg cagccggaca acgggctgca
 851  atggtcgccg tggtttcgca tcatcgccgc gcgcttcctt gagcgttggt
 901  gggctgacct ggacgcggcc ctaaacactg acaaacacga ggattgggga
 951  acggtgcatc acatcaacga agcgtgaaag cagaagctgc aggatgtgaa
1001  gacacgtcat ggggtggaat tgcgtacttg gcagcttcgt atctcctttt
1051  tctgagactg aacctgcagt caggtcccac aaggtcaggt aaaatggctc
1101  gataaaatgt accgtcactt tttgtcgcgt atactgaact ccaagaggtc
1151  aaaaaaaaaa aaaaa
```

FIG. 18B

Haematococcus pluvialis Ipi2

```
   1 tggaacctgg cccggcggca gtccgatgcc gcgatgcttc gttcgttgct
  51 cagaggcctc acgcatatcc cgcgcgtgaa ctccgcccag cagcccagct
 101 gtgcacacgc gcgactccag tttaagctca ggagcatgca gctgcttgcc
 151 gaggaccgca cagaccacat gaggggtgca agcacctggg caggcgggca
 201 gtcgcaggat gagctgatgc tgaaggacga gtgcatctta gtggatgctg
 251 acgacaacat cacaggccat gccagcaagc tggagtgcca caaattccta
 301 ccacatcagc ctgcaggcct gctgcaccgg gccttctctg tgttcctgtt
 351 tgacgaccag gggcgactgc tgctgcaaca gcgtgcacgc tcaaaaatca
 401 ccttcccaag tgtgtggacg aacacctgct gcagccaccc tctacatggg
 451 cagaccccag atgaggtgga ccaactaagc caggtggccg acggcacagt
 501 acctggcgca aaagctgctg ccatccgcaa gttggagcac gagctgggga
 551 taccagcgca ccagctgccg gcaagcgcgt ttcgcttcct cacgcgtttg
 601 cactactgtg ccgcggacgt gcagccggct gcgacacaat cagcgctctg
 651 gggcgagcac gagatggact acatcttatt catccgggcc aacgtcacct
 701 tggcgcccaa ccctgacgag gtggacgaag tcaggtacgt gacgcaagag
 751 gagctgcggc agatgatgca gccggacaac gggttgcaat ggtcgccgtg
 801 gtttcgcatc atcgccgcgc gcttccttga gcgttggtgg gctgacctgg
 851 acgcggccct aaacactgac aaacacgagg attggggaac ggtgcatcac
 901 atcaacgaag cgtgaaggca gaagctgcag gatgtgaaga cacgtcatgg
 951 ggtggaattg cgtacttggc agcttcgtat ctcctttttc tgagactgaa
1001 cctgcagagc tagagtcaat ggtgcatcat attcatcgtc tctcttttgt
1051 tttagactaa tctgtagcta gagtcactga tgaatccttt acaactttca
1101 aaaaaaaaa
```

FIG. 19A

Lactuca sativa Ipi1

```
  1 tgccaaaatg ttgaaatttc ccccttttaa aaccattgct accatgatct
 51 cttctccata ttcttccttc ttgctgcctc ggaaatcttc tttccctcca
101 atgccgtctc tcgcagccgc tagtgttttc ctccaccctc tttcgtctgc
151 cgctatgggc gattccagca tggatgctgt ccagcgacgt ctcatgttcg
201 atgacgaatg cattttggtg gatgagaatg acaaagtggt tggccatgat
251 actaaataca attgtcattt gatggagaag attgaaaagg gaaatatgct
301 acacagagca ttcagtgtgt tcttgttcaa ctcgaaatat gaattactcc
351 ttcagcaacg ttctgcaacc aaggtgactt tccctttggt atggacaaac
401 acgtgttgca gccatccact atacagggag agtgagctta ttgacgaaaa
451 cgcccttggg gtgaggaatg ctgcacagag gaagctcctg gatgaactcg
501 gcatccctgg agcagatgtt ccggttgatg agttcactcc attgggtcgc
551 attctataca aggccgcatc ggatggaaag tggggagaac atgaacttga
601 ttacctgctg tttatggtac gtgatgttgg tttggatccg aacccagatg
651 aagtgaaaga tgtaaaatat gtgaaccggg aagagctgaa ggaattggta
701 aggaaggcgg atgctggtga agagggtgtg aagctgtccc cgtggttcaa
751 attgattgtc gataatttct tgtttcagtg gtgggatcga ctccataagg
801 gaaccctaac cgaagctatt gatatgaaaa caatccacaa actcacataa
851 aaacactaca ctagtaggag agaggattat atgagatatt tgttatatgt
901 gaaattgaaa ttcagatgaa tgcttgtatt tatttctatt tggacaaact
951 tcaacttctt tttgctacct tatcagaaaa aaaaa
```

FIG. 19B

Lactuca sativa Ipi2

```
  1 tattcgcttc aaaatctctt ccattaactg ctcaaatctc caccttcgcc
 51 ggtcttaatc tccgccggcg cactttcacc accataaccg ccgccatggg
101 tgacgattcc ggcatggacg ctgtccagag acgtctcatg tttgatgatg
151 aatgcatttt ggttgatgaa aatgacaatg ttcttgggca tgataccaaa
201 tacaattgtc acttgatgga gaagattgag aaagataatt tgcttcatag
251 agcattcagt gtatttttat tcaattcaaa atacgaatta ctccttcagc
301 aaaggtcaga aaccaaggtg acatttcctt tggtatggac aaacacctgt
351 tgcagccatc cactatacag agaatcggag ttaattcccg aaaatgccct
401 tggggtcaga aatgctgcac agaggaagct tctagatgaa ctcggtatcc
451 ctgctgaaga tgttccagtt gatgagttca caactttagg tcgcatgttg
501 tacaaggctc catctgatgg aaaatggggt gaacatgaag ttgattacct
551 actcttcctc gtgcgtgacg ttgccgtgaa cccaaaccct gatgaggtgg
601 cggacattag atacgtgaac caagaagagt taaaagagtt actaaggaag
651 gcggatgcgg gtgaggaggg tttgaaattg tccccatggt ttaggctagt
701 ggtggacaac ttcttgttca aatggtggga tcatgtccaa aaggggacac
751 tcaatgaagc aattgacatg aaaaccattc ataagttgat atgaaaaatg
801 gttaatattt atggtggtgg tttggagcta ataatttgtg tgttcaagtc
851 tcggtccttc ttttttaac gtttttttt tttcttttat tgggagtgtt
901 tattgtgtac ttgtaacgta ggccctttgg ttacgcttta agagtttaat
951 aaagaaccac cgttaattta aaaaaaaaaa aaaaaaaa
```

FIG. 20

Chlamydomonas reinhardtii Ipi1

(Note: the isomerase cDNA probably ends at ca. base 1103; the second half of the cDNA is similar to extensin and other hydroxyproline-rich structural proteins)

```
   1 ggcacgagct cgagtttgtt ttaccatgac atcgggaatt tggaagcttg
  51 aactacctca attactcaag taactcgcgg caacacattt cgcgcgccat
 101 cgctgttttc tctgctccag ctaccgagca gcattgcttt agatcgcttt
 151 gatgtcataa actcccactt atatgagatc cagtttcatc gagcccaagc
 201 ccagagcgca acctgtctta agccgcggca gggcgtccat gcgcctcgcg
 251 caaagccgtg ctctcgttgc gcgtgtcagc tccgccctgt ggccgggagc
 301 aggactttca caggctcaaa gcgttgcggt gcgaatggcg agttcgtcaa
 351 cctgggaagg cacgggcctg agccaggatg acttcatgca gcgggacgag
 401 tgcttggtgg tggacgagca ggaccggctg ctaggcaccg ccaacaagta
 451 cgactgccac cgcttcgagg cggccaaggg ccagccctgc ggccgcctgc
 501 accgcgcctt ctccgtgttc ctgttcagcc ccgacggccg actgctgctg
 551 cagcagcgcg cagccagcaa ggtgacgttc ccgggtgtgt ggaccaacac
 601 ctgctgctcg cacccgctgg cgggccaggc gccggacgag gtggacctgc
 651 cggcggcggt agcctcgggc caggtgccgg gcatcaaggc ggcggcggtg
 701 cgcaagctgc agcacgagct ggggataccg ccggagcagg ttcccgcctc
 751 ctccttctcc ttcctcacgc gtctgcacta ctgcgccgcc gacaccgcca
 801 cgcacggccc ggcggcggag tggggcgagc acgaggtgga ctacgtgctg
 851 ttcgtgcggc cgcagcagcc cgtcagcctg cagcccaacc cagacgaggt
 901 ggacgccacg cgctacgtga cgctgccgga gcttcagtcc atgatggcgg
 951 accccggcct cagctggagc ccctggttcc gcatcctggc cacacagccc
1001 gccttcctgc ccgcctggtg ggcgacctg aagcggcgct ggcgcccggg
1051 cggcagccga ctgtaggact ggggcaccat ccaccgcgtc atgtgaagaa
1101 aaaggggaag caggggcggg agcgggggat gaatgggaat gtgaatgcga
1151 ttgtgatgcg gcgtgggatg aggtctgaag acagggggaa aatcgggggg
1201 cgggcgtgag cgtgtgtgta cgtgagcgac aaagccggga ggcggaccgc
1251 gcgatgggta catgtgtgtg cggagggtcg gtgggtcggt cggttgcgcg
1301 gcatagcgtg ttgtgtgtgt gcggctgcgc gggtatgtgg gcacccgggc
1351 acggaggaga aggcacacgc aggtggcgcg gaggtgtgtc aggggccatg
1401 ggcgggcctc actcctggtc gtgcccagtg gtctcgtggg cagagtggca
1451 ggggctgcac ccatatgagc ggcgcactgc cgcgctgggc taagtcctta
1501 tcacttggtg aggtggggcg aggtggctgt gggcggcggg cgcagtggca
1551 gaaggacacg gtgtgtgagc ggtggagctc tggccgtgcc ggccgtgagg
1601 ggcggatagc gatatgacgt tgtgcttggc cgctgtaatg cgggagaatg
1651 tgcaggccgc gagaagcggg cggtggcagg aggccgcagg ctgcagcacc
1701 cgttggggag gtgccgcctg caggcgcggc gccgggcggg cctgagtaat
1751 gggcgcctga gtagtggcgg ccacaggagg cgcaggaggc agcagcagga
1801 ggacgagctg gagggacccg ttggcaaccc aaggttgcgc gtgtaacata
1851 gtggccatac aaaaaaaaaa aaaa
```

FIG. 21A

Tagetes erecta Ipi1

```
  1 ccaaaaacaa ctcaaatctc ctccgtcgct cttactccgc catgggtgac
 51 gactccggca tggatgctgt tcagcgacgt ctcatgtttg acgatgaatg
101 cattttggtg gatgagtgtg acaatgtggt gggacatgat accaaataca
151 attgtcactt gatggagaag attgaaacag gtaaaatgct gcacagagca
201 ttcagcgttt ttctattcaa ttcaaaatac gagttacttc ttcagcaacg
251 gtctgcaacc aaggtgacat ttcctttagt atggaccaac acctgttgca
301 gccatccact ctacagagaa tccgagcttg ttcccgaaaa cgcccttgga
351 gtaagaaatg ctgcacagag gaagctgttg gatgaactcg gtatccctgc
401 tgaagatgtt cccgttgatc agtttactcc tttaggtcgc atgctctaca
451 aggctccatc tgatggaaag tggggagaac atgaacttga ctacctactt
501 ttcatagtga gagacgttgc tgtaaacccg aacccagatg aagtggcgga
551 tatcaaatat gtganccang aagagttaaa ggagctgcta aggaaagcag
601 atgcgggggga ggagggtttg aagctgtctc catggttcag gttagtggtt
651 gataacttct tgttcaagtg gtgggatcat gtgcaaaagg gtacactcac
701 tgaagcaatt gatatgaaaa ccatacacaa gctgatatag aaacacaccc
751 tcaaccgaaa agttcaagcc taataattcg ggttgggtcg ggtctaccat
801 caattgtttt tttcttttaa gaagttttaa tctctatttg agcatgttga
851 ttcttgtctt ttgtgtgtaa gattttgggt ttcgtttcag ttgtaataat
901 gaaccattga tggtttgcaa tttcaagttc ctatcgacat gtagtgatct
951 aaaaaa
```

FIG. 21B

Oryza sative Ipi1

```
   1 cctccctttg cctcgcgcag aggcggccgc gccttctccg ccgcgaggat
  51 ggccggcgcc gccgccgccg tggaggacgc cgggatggac gaggtccaga
 101 agcggctcat gttcgacgac gaatgcattt tggtggatga acaagacaat
 151 gttgttggcc atgaatcaaa atataactgc catctgatgg aaaaaatcga
 201 atctgaaaat ctacttcata gggctttcag tgtattcctg ttcaactcaa
 251 aatatgaact cctactccag caacgatctg caacaaaggt tacatttcct
 301 ctagtttgga ccaacacttg ctgcagccat cctctgtacc gtgagtctga
 351 gcttatacag gaaaactacc ttggtgttag aaatgctgct cagaggaagc
 401 tcttggatga gctgggcatc ccagctgaag atgtgccagt tgaccaattc
 451 acccctcttg gtcggatgct ttacaaggcc ccatctgatg gaaaatgggg
 501 tgaacacgag cttgactacc tgctgttcat cgtccgcgac gtgaaggtag
 551 tcccgaaccc ggacgaagtg gccgatgtga aatacgtgag ccgtgagcag
 601 ctgaaggagc tcatccgcaa agcggacgcc ggagaggaag gcctgaagct
 651 gtctccctgg ttccggctgg ttgttgacaa cttcctcatg ggctggtggg
 701 atcacgtcga gaaaggcacc ctcaacgagg ccgtggacat ggagaccatc
 751 cacaagctga agtaaggact gcgatgttgt ggctggaaag aatgatcctg
 801 aagactctgt tcttgtgctg ctgcatatta ctcttaccag ggaagttgca
 851 gaagtcagaa gaagcttttg tatgtttctg ggtttggagc ttggaagtgt
 901 tgggctctgc tgactgagag attcccttat agagtgtcta tgttaattta
 951 gcaaacttct atattataca tgattagtta attgttcggt gtctgaataa
1001 agaacaatag catgttccat gtttatttgc t
```

ClustalW 1.7 Multiple Sequence Alignment of Plant and Green Algal Isopentenyl Pyrophosphate Isomerases (IPI)
These amino acid sequences were predicted by cDNAs that were isolated and identified by color complemtation in *E.coli*

```
                   1             15 16           30 31           45 46           60 61           75 76           90
 1 T.erecta 1      --------------- --------------- --------------- --------------- -MGD--DSGMDAVQR RLMFDDECILVDECD   27
 2 L.sativa 1      --------MLKFPPF KTIATMISSPYSSFL LPRKSSFPPMPS--- -LAAASVFLHPLSSA AMGD--SS-MDAVQR RLMFDDECILVDEND   75
 3 L.sativa 2      --------------- --------------- --------------- --------------- -MGD--DSGMDAVQR RLMFDDECILVDEND   27
 4 A.palaestina 2  MSSIRINPLYSIFST TTKTLSASCSSPAVH LQQRCRTLSISSSIT NSPRRGLNRLFASTS TMGEVADAGMDAVQK RLMFDDECILVDEND   90
 5 A.palaestina 1  --------------- --------------- --------------- --------------- -MGEVTDAGMDAVQK RLMFDDECILVDEND   29
 6 O.sativa 1      --------------- --------------- --------------- ------------MAG AAAAVEDAGMDEVQK RLMFDDECILVDEQD   33
 7 A.thaliana 1    ---MSVSSLFNLPLI RLRSLALSSSFSSFR FAHRP--LSSIS--- --PRKLPNFRAFSGT AMTDTKDAGMDAVQR RLMFEDECILVDETD   80
 8 A.thaliana 2    --------------- --------------- --------------- --------------- -MTDSNDAGMDAVQR RLMFEDECILVDENN   29
 9 H.pluvialis 1   ---MLRSLLRGLTHI PRVNSAQQPSCAHAR LQFKLRSMQLLS--- ---------EDRTDH MRGASTWAG-GQSQD ELMLKDECILVDVED   74
10 H.pluvialis 2   ---MLRSLLRGLTHI PRVNSAQQPSCAHAR LQFKLRSMQMTLMQP SISANLSRAEDRTDH MRGASTWAG-GQSQD ELMLKDECILVDVED   86
11 C.reinhardtii 1 ---MRSSFIE---PK PRAQPVLSRGRASMR LAQSRALVARVSSAL WPGAGLSQAQSVAVR MASSSTWEGTGLSQD DFMQRDECLVVDEQD   84

                   91           105 106         120 121         135 136         150 151         165 166         180
 1 T.erecta 1      NVVGHDTKYNCHLME KIE--TGKMLHRAFS VFLENSKYELLLQQR SATKVTFPLVWTNTC CSHPLYRES------ --ELVPENALGVRNA  107
 2 L.sativa 1      KVVGHDTKYNCHLME KIE--KGNMLHRAFS VFLENSKYELLLQQR SATKVTFPLVWTNTC CSHPLYRES------ --ELIDENALGVRNA  155
 3 L.sativa 2      NVLGHDTKYNCHLME KIE--KDNLLHRAFS VFLFNSKYELLLQQR SETKVTFPLVWTNTC CSHPLYRES------ --ELIPENALGVRNA  107
 4 A.palaestina 2  KVVGYDSKYNCHLME KIE--AENLLNRAFS VFLFNSKYELLLQQR SATKVTFPLVWTNTC CSHPLFRDS------ --ELIEENFLGVRNA  170
 5 A.palaestina 1  KVVGHDSKYNCHLME KIE--AENLLHRAFS VFLFNSKYELLLQQR SATKVTFPLVWTNTC CSHPLFRDS------ --ELIEENYLGVRNA  109
 6 O.sativa 1      NVVGHESKYNCHLME KIE--SENLLHRAFS VFLFNSKYELLLQQR SATKVTFPLVWTNTC CSHPLYRES------ --ELIQENYLGVRNA  113
 7 A.thaliana 1    RVVGHVSKYNCHLME NIE--AKNLLHRAFS VFLFNSKYELLLQQR SNTKVTFPLVWTNTC CSHPLYRES------ --ELIQDNALGVRNA  160
 8 A.thaliana 2    RVVGHDTKYNCHLME KIE--AENLLHRAFS VFLFNSKYELLLQQR SKTKVTFPLVWTNTC CSHPLYRES------ --ELIEENVLGVRNA  109
 9 H.pluvialis 1   NITGNASKLECHKFL PH--QPAGLLHRAFS VFLFDDQGRLLLQQR ARSKITFPSVWTNTC CSHPLHGQTPDEVDQ LSQVADGTVPGAKAA  162
10 H.pluvialis 2   NITGHASKLECHKFL PH--QPAGLLHRAFS VFLFDDQGRLLLQQR ARSKITFPSVWTNTC CSHPLHGQTPDEVDQ LSQVADGTVPGAKAA  174
11 C.reinhardtii 1 RLLGTANKYDCHRFE AAKGQPCGRLHRAFS VFLFSPDGRILLQQR AASKVTFPGVWTNTC CSHPLAGQAPDEVDL PAAVASGQVPGIKAA  174
```

FIG. 22A

```
                    181           195 196           210 211           225 226           240 241           255 256           270
1 T.erecta 1        AQRKLLDELGIPAED VPVDQFTPLGRMLY- --KAPSDG----KWG EHELDYLLFIVRD-- VAVNPNPDEVADIKY VSHEELKELLRKADA   188
2 L.sativa 1        AQRKLLDELGIPGAD VPVDEFTPLGRILY- --KAASDG----KWG EHELDYLLFMVRD-- VGLDPNPDEVKDVKY VNREELKELVRKADA   236
3 L.sativa 2        AQRKLLDELGIPAED VPVDEFTTLGRMLY- --KAPSDG----KWG EHEVDYLLFLVRD-- VAVNPNPDEVADIRY VNQEELKELLRKADA   188
4 A.palaestina 2    AQRKLLDELGIPAED VPVDEFTPLGRILY- --KAPSDG----KWG EHELDYLLFIVRD-- VKYDPNPDEVADAKY VNREELKEILRKADA   251
5 A.palaestina 1    AQRKLLDELGIPAED VPVDEFTPLGRILY- --KAPSDG----KWG EHELDYLLFIVRD-- VKYDPNPDEVADAKY VNREELREILRKADA   190
6 O.sativa 1        AQRKLLDELGIPAED VPVDQFTPLGRMLY- --KAPSDG----KWG EHELDYLLFIVRD-- VKVVPNPDEVADVKY VSREQLKELIRKADA   194
7 A.thaliana 1      AQRKLLDELGIVAED VPVDEFTPLGRMLY- --KAPSDG----KWG EHELDYLLFIVRD-- VKVQPNPDEVAEIKY VSREELKELVKKADA   241
8 A.thaliana 2      AQRKLFDELGIVAED VPVDEFTPLGRMLY- --KAPSDG----KWG EHEVDYLLFIVRD-- VKLQPNPDEVAEIKY VSREELKELVKKADA   190
9 H.pluvialis 1     AIRKLEHELGIPAHQ LPASAFRFLTRLHYC AADVQPAATQSALWG EHEMDYILFIRAN-- VTLAPNPDEVDEVRY VTQEELRQMMQP---   247
10 H.pluvialis 2    AIRKLEHELGIPAHQ LPASAFRFLTRLHYC AADVQPAATQSALWG EHEMDYILFIRAN-- VTLAPNPDEVDEVRY VTQEELRQMMQP---   259
11 C.reinhardtii 1  AVRKLQHELGIPPEQ VPASSFSFLTRLHYC AADTATHG-PAAEWG EHEVDYVLFVRPQQP VSLQPNPDEVDATRY VTLPELQSMMA----   259

                    271           285 286           300 301           315 316
1 T.erecta 1        GEEGLKLSPWFRLVV DN--FLFKWWDHVQK GTL---TEAIDMKTI HKLI--   232  Tagetes erecta (marigold)
2 L.sativa 1        GEEGVKLSPWFKLIV DN--FLFQWWDRLHK GTL---TEAIDMKTI HKLT--   280  Lactuca sativa (romaine lettuce)
3 L.sativa 2        GEEGLKLSPWFRLVV DN--FLFKWWDHVQK GTL---NEAIDMKTI H-----   229  Lactuca sativa (romaine lettuce)
4 A.palaestina 2    GEEGIKLSPWFRLVV DN--FLFKWWDHVEE GKI---KDVADMKTI HKLT--   295  Adonis palaestina (pheasant's eye)
5 A.palaestina 1    GEEGLKLSPWFRLVV DN--FLFKWWDHVEQ GTI---KEVADMKTI HKLT--   234  Adonis palaestina (pheasant's eye)
6 O.sativa 1        GEEGLKLSPWFRLVV DN--FLMGWWDHVEK GTL---NEAVDMETI HKLK--   238  Oryza sativa (rice)
7 A.thaliana 1      GEEGLKLSPWFRLVV DN--FLMKWWDHVEK GTL---VEAIDMKTI HKL---   284  Arabidopsis thaliana
8 A.thaliana 2      GDEAVKLSPWFRLVV DN--FLMKWWDHVEK GTI---TEAADMKTI HKL---   233  Arabidopsis thaliana
9 H.pluvialis 1     -DNGLQWSPWFRIIA AR--FLERWWADLDA ALN--TDKHEDWGTV HHINEA   293  Haematococcus pluvialis
10 H.pluvialis 2    -DNGLQWSPWFRIIA AR--FLERWWADLDA ALN--TDKHEDWGTV HHINEA   305  Haematococcus pluvialis
11 C.reinhardtii 1  -DPGLSWSPWFRILA TQPAFLPAWWGDLKR RWRPGGSRLSDWGTI HRVM--   307  Chlamydomonas reinhardtii
```

FIG. 22B

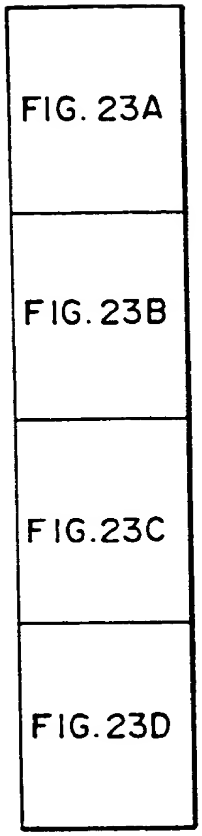


FIG. 23

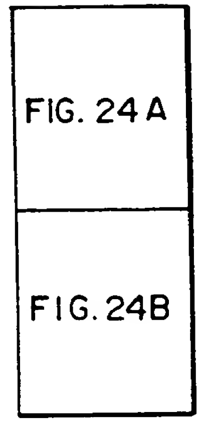


FIG. 24

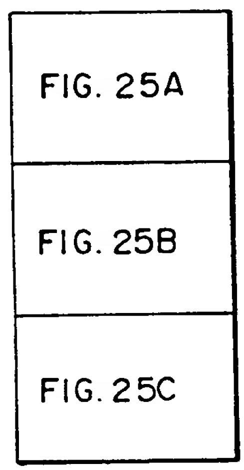


FIG. 25

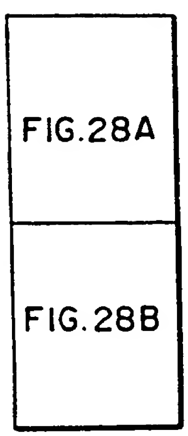


FIG. 28

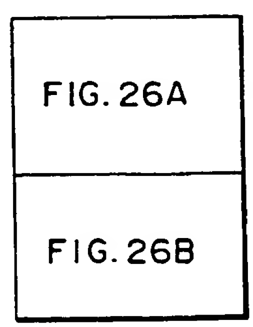


FIG. 26

FIG. 23A

Comparison using GAP program of the Genetics Computer Group

Gap Weight:	50	Average match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	17392	Length:	1904
Ratio:	9.411	Gaps:	3
Percent Similarity:	95.331	Percent Identity:	95.331

Match display thresholds for the alignment(s):
| = IDENTITY : = 5 . = 1

Adonis palaestina ε-cyclase #3 x *Adonis palaestina* ε-cyclase #5

```
             .         .         .         .         .
  1 gagagaaaaagagtgttatattaatgttactgtcgcattcttgcaacac. 49
          ||| ||||||| |||||||||||||||||||||||||||||||
  1 ......aaaggagtgttctattaatgttactgtcgcattcttgcaacact 44

             .         .         .         .         .
 50 .atattcagactccattttcttgttttctcttcaaaacaacaaactaatg 98
     ||||||| ||||||||||||| |||||||||||||||||||||||||||
 45 tatattcaaactccattttcttcttttctcttcaaaacaacaaactaatg 94

             .         .         .         .         .
 99 tga.cggagtatctagctatggaactacttggtgttcgcaacctcatctc 147
    ||| | |||||||| |||||||||||||||||||||||||||||||||||
 95 tgagcagagtatctggctatggaactacttggtgttcgcaacctcatctc 144

             .         .         .         .         .
148 ttcttgccctgtctggacttttggaacaagaaaccttagtagttcaaaac 197
    |||||||||||| |||||||||||||||||||||||||||||||||||||
145 ttcttgccctgtgtggacttttggaacaagaaaccttagtagttcaaaac 194

             .         .         .         .         .
198 tagcttataacatacatcgatatggttcttcttgtagagtagattttcaa 247
    ||||||||||||||||||||||||||||||||||||||||||||||||||
195 tagcttataacatacatcgatatggttcttcttgtagagtagattttcaa 244

             .         .         .         .         .
248 gtgagggctgatggtggaagcgggagtagaacttctgttgcttataaaga 297
    ||||| ||||||||||||||||||||||||| ||||||||||||||||||
245 gtgagagctgatggtggaagcgggagtagaagttctgttgcttataaaga 294

             .         .         .         .         .
298 gggttttgtggacgaggaggattttatcaaagctggtggttctgagcttt 347
    |||||||||||| |  ||||||||||||||||||||||||||||||||||
295 gggttttgtggatgaagaggattttatcaaagctggtggttctgagcttt 344

             .         .         .         .         .
348 tgtttgtccaaatgcagcaaacaaagtctatggagaaacaggccaagctc 397
    ||||||||||||||||||||||||||||||||||||||||||||||||||
345 tgtttgtccaaatgcagcaaacaaagtctatggagaaacaggccaagctc 394
```

FIG. 23B

```
398 gccgataagttgccaccaatacctttcggagaatctgtgatggacttggt 447
    |||||||||||||||||||||||||| |||||||| ||||||||||||||
395 gccgataagttgccaccaatacctttggagaatccgtgatggacttggt 444

448 tgtaataggttgtggacctgctggtctttcactggctgcagaagctgcta 497
    ||||||||||||||||||||||||||||||||||||||||||||||||||
445 tgtaataggttgtggacctgctggtctttcactggctgcagaagctgcta 494

498 agctaggcttgaaagttggccttattggtcctgatcttccttttacaaat 547
    ||||||| ||||||||||||||||||||||||||||||||||||||||||
495 agctagggttgaaagttggccttattggtcctgatcttccttttacaaat 544

548 aattatggtgtgtgggaagacgagttcaaagatcttggacttgaacgttg 597
    ||||||||||||||||||||||||||||||||||||||||||||||||||
545 aattatggtgtgtgggaagacgagttcaaagatcttggacttgaacgttg 594

598 tatcgagcatgcttggaaggacaccatcgtatatcttgacaatgatgctc 647
    ||||||||||||||||||||||||||||||||||||||| ||||||||||
595 tatcgagcatgcttggaaggacaccatcgtatatcttgataatgatgctc 644

648 ctgtccttattggtcgtgcatatggacgagttagccggcatttgctgcat 697
    |||||||||||||||||||||||||||||||||| || |||||||| |||
645 ctgtccttattggtcgtgcatatggacgagttagtcgacatttgctacat 694

698 gaagagttgctgaaaaggtgtgtcgagtcaggtgtatcatatctgaattc 747
    || |||||||||||||||||||| ||||||||||||||||||||| ||||
695 gaggagttgctgaaaaggtgtgtggagtcaggtgtatcatatctggattc 744

748 taaagtggaaaggatcactgaagctggtgatggccatagtcttgtagttt 797
    ||||||||||||||||||||||||||||||||||||||| ||||||||||
745 taaagtggaaaggatcactgaagctggtgatggccatagccttgtagttt 794

798 gtgaaaacgacatctttatcccttgcaggcttgctactgttgcatctgga 847
    ||||||| || |||||||||||||||||||||||||||||||||||||||
795 gtgaaaatgagatctttatcccttgcaggcttgctactgttgcatctgga 844

848 gcagcttcagggaaacttttggagtatgaagtaggtggccctcgtgtttg 897
    ||||||||||||||||||||||||||||||||||||||||||||||||||
845 gcagcttcagggaaacttttggagtatgaagtaggtggccctcgtgtttg 894

898 tgtccaaactgcttatggtgtggaggttgaggtggagaacaatccatacg 947
    ||||||||| |||||||| |||||||||||||||||||||||||||||||
895 tgtccaaaccgcttatggggtggaggttgaggtggagaacaatccatacg 944
```

FIG. 23C

```
 948 atcccaacttaatggtatttatggactacagagactatatgcaacagaaa  997
     ||||||||||||||||||| ||||||||||||||||||||||||||||||
 945 atcccaacttaatggtattcatggactacagagactatatgcaacagaaa  994

 998 ttacagtgctcggaagaagaatatccaacatttctctatgtcatgcccat 1047
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 995 ttacagtgctcggaagaagaatatccaacatttctctatgtcatgcccat 1044

1048 gtcgccaacaagactttttttgaggaaacctgtttggcctcaaaagatg 1097
     |||||||||||||||||||||||||||||||||||||||||||||||||
1045 gtcgccaacaagactttttttgaggaaacctgtttggcctcaaaagatg 1094

1098 ccatgcctttcgatctactgaagagaaaactaatgtcacgattgaagact 1147
     ||||||| |||||||||||||||||||||||| |||||||||||||||||
1095 ccatgccattcgatctactgaagagaaaactgatgtcacgattgaagact 1144

1148 ctgggtatccaagttacaaaaatttatgaagaggaatggtcttatattcc 1197
     ||||||||||||||||||||| ||||||||||||||||||| ||||||||
1145 ctgggtatccaagttacaaaagtttatgaagaggaatggtcatatattcc 1194

1198 tgttggggttctttaccaaacacagagcaaaagaacctagcatttggtg 1247
     |||||| ||||||||||||||||||||||||||||||||||||||||||
1195 tgttggtggttctttaccaaacacagagcaaaagaacctagcatttggtg 1244

1248 ctgcagcaagcatggtgcatccagcaacaggctattcggttgtacgatca 1297
     |||||||||||||||||||||||||||||||||||||||||||||| |||
1245 ctgcagcaagcatggtgcatccagcaacaggctattcggttgtacggtca 1294

1298 ctatcagaagctccaaaatatgcttctgtaattgcaaagatttgaagca 1347
     || ||||||||||||||||||||||||||||||||||||||||||||||
1295 ctgtcagaagctccaaaatatgcttctgtaattgcaaagatttgaagca 1344

1348 agataactctgcatatgtggtttctggacaaagcagtgcagtaaacattt 1397
     |||||||||| |||||||||||||||||||| ||||||||||||||||||
1345 agataactctgcgtatgtggtttctggacaaagtagtgcagtaaacattt 1394

1398 caatgcaagcatggagcagtctttggccaaaggagcgaaaacgtcaaaga 1447
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1395 caatgcaagcatggagcagtctttggccaaaggagcgaaaacgtcaaaga 1444

1448 gcattctttcttttcgggttagagcttattgtgcagctagatattgaagc 1497
     |||||||||||||| || ||||||||||||||||||||||||||||||||
1445 gcattctttcttttggattagagcttattgtgcagctagatattgaagc 1494
```

```
1498 aaccagaacgttctttagaaccttcttccgcttgccaacttggatgtggt 1547
     ||||||||| ||||||||||||||||||||||||||||||||||||||||
1495 aaccagaacattctttagaaccttcttccgcttgccaacttggatgtggt 1544

1548 ggggtttccttgggtcttcactatcatctttcgatcttgtattgttttcc 1597
     ||||||||||||||||||||||||||||||||||||| || |||||||||
1545 ggggtttccttgggtcttcactatcatctttcgatctcgtcttgttttcc 1594

1598 atgtacatgtttgttttggccccgaacagcatgaggatgtcacttgtgag 1647
     |||||||||||||||||||| || ||||||||||||||||||||||||||
1595 atgtacatgtttgttttggcgccaaacagcatgaggatgtcacttgtgag 1644

1648 acatttgctttcagatccttctggtgcagttatggttaaagcttacctcg 1697
     |||||||||||||||||||||||||||||||||||| | | |||||||||
1645 acatttgctttcagatccttctggtgcagttatggtaagagcttacctcg 1694

1698 aaaggtaatc...tgttttatgaaactatagtgtctcattaaataaatga 1744
     ||||||| ||   | | |||| ||||| |||||| |||  |||||||||||
1695 aaaggtagtctcatctattattaaactctagtgtttcaccaaataaatga 1744

1745 ggatccttcgtatatgtatatgatcatctctatgtatatcctatattcta 1794
     |||||||||| || |||||||||||||||||||||||||||| || ||||
1745 ggatccttcgaatgtgtatatgatcatctctatgtatatcctgtactcta 1794

1795 atctcataaagtaatcgaaaattcattgatagaaaaaaaaaaaaaaaaaa 1844
     ||||||||||||||  |     |     || |       |||      ||
1795 atctcataaagtaaatgccgggtttgatattgttgtgtcaaaccggccaa 1844

1845 aaaa.............................................. 1848
       |
1845 tgatataaagtaaatttattgatacaaaagtagtttttttttttaaaaaa 1894
```

FIG. 23D

FIG. 24A

GAP program of Genetics Computer Group
blosum62.cmp

```
           Gap Weight:     12          Average Match:    2.912
        Length Weight:      4        Average Mismatch:  -2.003
              Quality:   2728                  Length:     530
                Ratio:  5,147                    Gaps:       0
   Percent Similarity: 99,623        Percent Identity:  99.057
Match display thresholds for the alignment(s):
              | = IDENTITY     : = 2     . = 1
```

Adonis palaestina ε-cyclase #3 x *Adonis palaestina* ε-cyclase #5

```
                .         .         .         .         .
   1 MELLGVRNLISSCPVWTFGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGG 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
   1 MELLGVRNLISSCPVWTFGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGG 50
                .         .         .         .         .
  51 SGSRTSVAYKEGFVDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPP 100
     ||||.|||||||||||||||||||||||||||||||||||||||||||||
  51 SGSRSSVAYKEGFVDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPP 100
                .         .         .         .         .
 101 IPFGESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWE 150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 101 IPFGESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWE 150
                .         .         .         .         .
 151 DEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKR 200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 151 DEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKR 200
                .         .         .         .         .
 201 CVESGVSYLNSKVERITEAGDGHSLVVCENDIFIPCRLATVASGAASGKL 250
     |||||||||.|||||||||||||||||||||:||||||||||||||||||
 201 CVESGVSYLDSKVERITEAGDGHSLVVCENEIFIPCRLATVASGAASGKL 250
                .         .         .         .         .
 251 LEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEE 300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 251 LEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEE 300
                .         .         .         .         .
 301 EYPTFLYVMPMSPTRLFFEETCLASKDAMPFDLLKRKLMSRLKTLGIQVT 350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 301 EYPTFLYVMPMSPTRLFFEETCLASKDAMPFDLLKRKLMSRLKTLGIQVT 350
```

```
             .         .         .         .         .
351 KIYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPK 400
    |:||||||||||||||||||||||||||||||||||||||||||||||||
351 KVYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPK 400

             .         .         .         .         .
401 YASVIAKILKQDNSAYVVSGQSSAVNISMQAWSSLWPKERKRQRAFFLFG 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 YASVIAKILKQDNSAYVVSGQSSAVNISMQAWSSLWPKERKRQRAFFLFG 450

             .         .         .         .         .
451 LELIVQLDIEATRTFFRTFFRLPTWMWWGFLGSSLSSFDLVLFSMYMFVL 500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 LELIVQLDIEATRTFFRTFFRLPTWMWWGFLGSSLSSFDLVLFSMYMFVL 500

             .         .         .
501 APNSMRMSLVRHLLSDPSGAVMVKAYLER* 530
    |||||||||||||||||||||||:||||||
501 APNSMRMSLVRHLLSDPSGAVMVRAYLER* 530
```

FIG. 24B

FIG. 25A

```
                      *        20         *        40         *        60         *        80         *       100         *
PotatoE        : -------------------------------------------------------------------------------------------------------------- :   -
ArabidopsisE   : MECVGARNF-AAMAVSTFPSWS-CRRKFPVVKRYSYRNIRFGL-CSV--RASGGGSSGSESCVAVREDF--ADEEDFVKAGGSEILFVQMQQNKDMDEQSKLVDKLPPIS : 103
AdonisE1       : MELLGVRNL-----ISSCPVWT-FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGSRSSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPIP : 102
AdonisE2       : MELLGVRNL-----ISSCPVWT-FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGSRTSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPIP : 102
LettuceEE      : MECFGARNMTATMAVFTCPRFTDCNIRHKFSLLKQRRFTNLSA-SSSLRQIKCSAKSDR--CVVDKQGISVADEEDYVKAGGSELFFVQMQRTKSMESQSKLSEKLAQIP : 107
TomatoE        : MECVGVQNV-GAMAVLTRPRLN----RWSGGELCQEKSIFLAY-EQY--ESKCNSSSGSDSCVVDKEDF--ADEEDYIKAGGSQLVFVQMQQKKDMDQQSKLSDELRQIS : 100
MarigoldE      : MSMRAG-HMTATMAAFTCPRFM-------------TSIRYT------KQIKCNAAKSQ---LVVKQEI--EEEEDYVKAGGSELLFVQMQQNKSMDAQSSLSQKLPRVP :  84
ArabidopsisB   : ------------------------------MDTLLKTPNKLDFFIPQFHGFE--RLCSNNPYHSRVRLGVKKRAIKIV------SSVVSGSAALLDLVPETKKENLDFEL :  72
AdonisB        : ------------------------------MDTLLRTHNKLELLPTLHGFA---EKQHLVSTSKLQNQVFRIASRNIH--PCRNGTVKARGSALLELVPETKKENLEFDL :  75
PepperB        : ------------------------------MDTLLRTPNNLEFL---HGFG---VKVSAFSSVKSQKFGAKKFCEGLG---SRSVCVKASSSALLELVPETKKENLDFEL :  71
TomatoB        : ------------------------------MDTLLKTPNNLEFLNPHHGF----AVKASTFRSEKHHNFGSRKFCETL---GRSVCVKGSSSALLELVPETKKENLDFEL :  73
TobaccoB       : ------------------------------MDTLLKTPNKLEFLHPVHGFS---VKASSFNSVKPHKFGSRKICENWG----KGVCVKAKSSALLELVPETKKENLDFEL :  73
MarigoldB      : ------------------------------MDTFLRTYNSFEFVHPSNKFAGNLNNLNQLNQSKSQFQDFRFGPKKSQFKLGQKYCVKASSSALLELVPEIKKENLDFDL :  80
DaffodilB      : ------------------------------MDTLLRTHNRLELLYPLHELA---KRHFLSPSPNPQNPNFKFFSRKPYQKKCRNGYIGVSSNQLLDLVPEIKKEHLEFDL :  77

                       120         *       140         *       160         *       180         *       200         *       220
PotatoE        : -------------------------------------------------------DEFKDLGLQACIEHVWRDTIVYLDDDDPILIGRAYGRVSRHLLHEELLKRCVEA :  54
ArabidopsisE   : IG-----DGALDHVVIGCGPAGLALAAESAKLGLKVGLIGPDLP---FTNNYGVWEDEFNDLGLQKCIEHVWRETIVYLDDDKPITIGRAYGRVSRRLLHEELLRRCVES : 205
AdonisE1       : FG-----ESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLP---FTNNYGVWEDEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKRCVES : 204
AdonisE2       : FG-----ESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLP---FTNNYGVWEDEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKRCVES : 204
LettuceEE      : IG-----NCILDLVVIGCGPAGLALAAESAKLGLNVGLIGPDLP---FTNNYGVWQDEFIGLGLEGCIEHSWKDTLVYLDDADPIRIGRAYGRVHRDLLHEELLRRCVES : 209
TomatoE        : AG-----QTVLDLVVIGCGPAGLALAAESAKLGLNVGLVGPDLP---FTNNYGVWEDEFKDLGLQACIEHVWRDTIVYLDDDEPILIGRAYGRVSRHFLHEELLKRCVEA : 202
MarigoldE      : IGGGGDSNCILDLVVIGCGPAGLALAGESAKLGLNVALIGPDLP---FTNNYGVWEDEFIGLGLEGCIEHVWRDTVVYLDDNDPILIGRAYGRVSRDLLHEELLTRCMES : 191
ArabidopsisB   : PLYDTSKSQVVDLAIVGGGPAGLAVAQQVSEAGLSVCSIDPS-PKLIWPNNYGVWVDEFEAMDLLDCLDTTWSGAVVYVDEGVKKDLSRPYGRVNRKQLKSKMLQKCITN : 181
AdonisB        : PAYDPSRGIVVDLAVVGGGPAGLAIAQQVSEAGLLVCSIDPS-PKLIWPNNYGVWVDEFEAMDLLDCLDTTWSGAVVYTDDNSKKYLDRPYGRVNRKQLKSKMLQKCVTN : 184
PepperB        : PMYDPSKGVVVDLAVVGGGPAGLAVAQQVSEAGLSVCSIDPN-PKLIWPNNYGVWVDEFEAMDLLDCLDATWSGAAVYIDDKTTKDLNRPYGRVNRKQLKSKMMQKCILN : 180
TomatoB        : PMYDPSKGVVVDLAVVGGGPAGLAVAQQVSEAGLSVCSIDPN-PKLIWPNNYGVWVDEFEAMDLLDCLDATWSGAAVYIDDNTAKDLHRPYGRVNRKQLKSKMMQKCIMN : 182
TobaccoB       : PMYDPSKGLVVDLAVVGGGPAGLAVAQQVSEAGLSVVSIDPS-PKLIWPNNYGVWVDEFEAMDLLDCLDATWSGTVVYIDDNTTKDLDRPYGRVNRKQLKSKMMQKCILN : 182
MarigoldB      : PMYDPSRNVVVDLVVVGGGPSGLAVAQQVSEAGLTVCSIDPS-PKLIWPNNYGVWVDEFEAMDLLDCLDTTWSSAVVYIDEKSTKSLNRPYARVNRKQLKTKMLQKCIAN : 189
DaffodilB      : PLYDPSKALTLDLAVVGGGPLARSCSTSLG-GGLSVVSIDPN-PKLIWPNNYGVWVDEFEDMDLLDCLDATWSGAIVYVDDRSTKNLSRPYARVNRKNLKSKMMKKCVSN : 185
```

```
                          *        240         *        260         *        280         *        300         *        320         *
PotatoE       : GVLYLNSKVDRIVEATNGHSLVECEGDVVIPCRFVTVASGAASGKFLQYELGGPRVSVQTAYGVEVEVDNNPFDPSLMVFMDYRDY---VRHDAQSLEAKYPTFLYAMPM : 161
ArabidopsisE  : GVSYLSSKVDSITEASDGLRLVACDDNNVIPCRLATVASGAASGKLLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVFMDYRDY---TNEKVRSLEAEYPTFLYAMPM : 312
AdonisE1      : GVSYLDSKVERITEAGDGHSLVVCENEIFIPCRLATVASGAASGKLLEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDY---MQQKLQCSEEEYPTFLYVMPM : 311
AdonisE2      : GVSYLNSKVERITEAGDGHSLVVCENDIFIPCRLATVASGAASGKLLEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDY---MQQKLQCSEEEYPTFLYVMPM : 311
LettuceEE     : GVSYLSSKVERITEAPNGYSLIECEGNITIPCRLATVASGAASGKFLEYELGGPRVCVQTAYGIEFEVENNPYDPDLMVFMDYRDF---SKHKPESLEAKYPTFLYVMAM : 316
TomatoE       : GVLYLNSKVDRIVEATNGQSLVECEGDVVIPCRFVTVASGAASGKFLQYELGSPRVSVQTAYGVEVEVDNNPFDPSLMFVMDYRDY---LRHDAQSLEAKYPTFLYAMPM : 309
MarigoldE     : GVSYLSSKVERITEAPNGLSLIECEGNITIPCRLATVASGAASGKLLQYELGGPRVCVQTAYGIEVEVESIPYDPSLMVFMDYRDY---TKHKSQSLEAQYPTFLYVMPM : 298
ArabidopsisB  : GVKFHQSKVTNVVH-EEANSTVVCSDGVKIQASVVLDATG-FSRCLVQYD-KPYNPGYQVAYGIVAEVDGHPFDVDKMVFMDWRDKHLDSYPELKERNSKIPTFLYAMPF : 288
AdonisB       : GVKFHQAKVIKVIH-EESKSLLICNDGITINATVVLDATG-FSRCLVQYD-KPYNPGYQVAYGIMAEVEEHPFDLDKMLFMDWRDSHLNEKLELKDKNRKIPTFLYAMPF : 291
PepperB       : GVKFHQAKVIKVIH-EESKSMLICNDGITIQATVVLDATG-FSRSLVQYD-KPYNPGYQVAYGILAEVEEHPFDVNKMVFMDWRDSHLKNNVELKERNSRIPTFLYAMPF : 287
TomatoB       : GVKFHQAKVIKVIH-EESKSMLICNDGITIQATVVLDATG-FSRSLVQYD-KPYNPGYQVAYGILAEVEEHPFDVNKMVFMDWRDSHLKNNTDLKERNSRIPTFLYAMPF : 289
TobaccoB      : GVKFHHAKVIKVIH-EEAKSMLICNDGVTIQATVVLDATG-FSRCLVQYD-KPYKPGYQVAYGILAEVEEHPFDTSKMVLMDWRDSHLGNNMELKERNRKVPTFLYAMPF : 289
MarigoldB     : GVKFHQAKVIKVIH-EELKSLLICNDGVTIQATLVLDATG-FSRSLVQYD-KPYNPGYQVAYGILAEVEEHPFDVDKMLFMDWRDSHLDQNLEIKARNSRIPTFLYAMPF : 296
DaffodilB     : GVRFHQATVVKAMH-EEEKSYLICSDGVTIDARVVLDATG-FSRCLVQYD-KPYNPGYQVAYGILAEVEEHPFDVDKMVFMDWRDSHLNGKAELNERNAKIPTFLYAMPF : 292

                     340         *        360         *        380         *        400         *        420         *        440
PotatoE       : SPTRVFFEETCLASKDAMPFDLLKKKLMLRLNTLGVRIKEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAPKCAFVLANILRQNHSKNMLTSS : 271
ArabidopsisE  : TKSRLFFEETCLASKDVMPFDLLKTKLMLRLDTLGIRILKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAEILREETTKQINS-- : 420
AdonisE1      : SPTRLFFEETCLASKDAMPFDLLKRKLMSRLKTLGIQVTKVYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAKILKQDNSAYVVSGQ : 421
AdonisE2      : SPTRLFFEETCLASKDAMPFDLLKRKLMSRLKTLGIQVTKIYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAKILKQDNSAYVVSGQ : 421
LettuceEE     : SPTKIFFEETCLASREAMPFNLLKSKLMSRLKAMGIRITRTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPNYAAVIAKILRQDQSKEMISLG : 426
TomatoE       : SPTRVFFEETCLASKDAMPFDLLKKKLMLRLNTLGVRIKEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAPKCASVLANILRQHYSKNMLTS- : 418
MarigoldE     : SPTKVFFEETCLASKEAMPFELLKTKLMSRLKTMGIRITKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPNYAAVIAKILGKGNSKQMLDHG : 408
ArabidopsisB  : SSNRIFLEETSLVARPGLRMEDIQERMAARLKHLGINVKRIEEDERCVIPMGGPLPVLPQRVVGIGGTAGMVHPSTGYMVARTLAAAPIVANAIVRYLGSPSSN-----S : 393
AdonisB       : SSTKIFLEETSLVARPGLRFEDIQERMVARLKHLGIKVKSIEEDERCVIPMGGPLPVLPQRVVGIGGTAGMVHPSTGYMVARTLAAAPVVAKSIVQYLGSDRSL------ : 395
PepperB       : SSNRIFLEETSLVARPGLGMDDIQERMVARLSHLGIKVKSIEEDEHCVIPMGGPLPVLPQRVVGIGGTAGMVHPSTGYMVARTLAAAPVVANAIIQYLSSERSH------ : 391
TomatoB       : SSNRIFLEETSLVARPGLRIDDIQERMVARLNHLGIKVKSIEEDEHCLIPMGGPLPVLPQRVVGIGGTAGMVHPSTGYMVARTLAAAPVVANAIIQYLGSERSH------ : 393
TobaccoB      : SSNKIFLEETSLVARPGLRMDDIQERMVARLNHLGIKVKSIEEDEHCVIPMGGSLPVIPQRVVGTGGTAGLVHPSTGYMVARTLAAAPVVANAIIHYLGSEKDL------ : 393
MarigoldB     : SSTRIFLEETSLVARPGLKMEDIQERMAYRLKHLGIKVKSIEEDERCVIPMGGPLPVLPQRVLGIGGTAGMVHPSTGYMVARTLAAAPIVAKSIIRYLNNEKSM---VAD : 403
DaffodilB     : SSNRIFLEETSLVARPGLKMEDIQERMVARLNHLGIRIKSIEEDERCVIPMGGPLPVIPQRVVGIGGTAGMVHPSTGYMVARTLAAAPIVANSIVQYLVSDSGL------ : 396
```

FIG. 25B

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                   *     240        *      260        *     280        *     300        *     320        *
PotatoE      : YLNSKVDRIVEATNGHSLVECEGDVVIPCRFVTVASGAASGKFLQYELGGPRVSVQTAYGVEVEVDNNPFDPSLMVFMDYRDYVRHDAQSLEAKYPTFLYAMPMSPTRVF : 167
ArabidopsisE : YLSSKVDSLTEASDGLRLVACDDNNVIPCRLATVASGAASGKLLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVFMDYRDYTNEKVRSLEAEYPTFLYAMPMTKSRLF : 318
AdonisE1     : YLDSKVERLTEAGDGHSLVVCENEIFIPCRLATVASGAASGKLLEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEEEYPTFLYVMPMSPTRLF : 317
AdonisE2     : YLNSKVERLTEAGDGHSLVVCENDIFIPCRLATVASGAASGKLLEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEEEYPTFLYVMPMSPTRLF : 317
LettuceEE    : YLSSKVERLTEAPNGYSLIECEGNITIPCRLATVASGAASGKFLQYELGGPRVCVQTAYGIEVEVENNPYDPDLMVFMDYRDFSKHKPESLEAKYPTFLYVMAMSPTKIF : 322
TomatoE      : YLNSKVDRIVEATNGQSLVECEGDVVIPCRFVTVASGAASGKFLQYELGSPRVSVQTAYGVEVEVDNNPFDPSLMVFMDYRDYLRHDAQSLEAKYPTFLYAMPMSPTRVF : 315

                  340        *     360        *     380        *     400        *     420        *     440
PotatoE      : FEETCLASKDAMPFDLLKKKLMLRLNTLGVRIKEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAPKCAFVLANILRQNHSKNMLTSSSTPS-I : 276
ArabidopsisE : FEETCLASKDVMPFDLLKTKLMLRLDTLGIRILKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAEILREETTKQINS------NI : 422
AdonisE1     : FEETCLASKDAMPFDLLKRKLMSRLKTLGIQVTKVYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAKILKQDNSAYVVSGQSSAVNI : 427
AdonisE1     : FEETCLASKDAMPFDLLKRKLMSRLKTLGIQVTKIYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAKILKQDNSAYVVSGQSSAVNI : 427
LettuceEE    : FEETCLASREAMPFNLLKSKLMSRLKAMGIRITRTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPNYAAVIAKILRQDQSKEMISLGKYT-NI : 431
TomatoE      : FEETCLASKDAMPFDLLKKKLMLRLNTLGVRIKEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAPKCASVLANILRQHYSKNMLTS-SSIPSI : 424
MarigoldE    : FEETCLASKEAMPFELLKTKLMSRLKTMGIRITKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPNYAAVIAKILGKGNSKQMLDHGRYTTNI : 414

                   *     460        *     480        *     500        *     520        *     540
PotatoE      : STQAWNTLWPQERKRQRSFFLFGLALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSXADLMLFAFYMFIIAPNDMRRGLIRHLLSDPTGATLIRTYLTF : 378
ArabidopsisE : SRQAWDTLWPPERKRQRAFFLFGLALIVQFDTEGIRSFFRTFFRLPKWMWQGFLGSTLTSGDLVLFALYMFVISPNNLRKGLINHLISDPTGATMIKTYLKV : 524
AdonisE1     : SMQAWSSLWPKERKRQRAFFLFGLELIVQLDIEATRTFFRTFFRLPTWMWWGFLGSSLSSFDLVLFSMYMFVLAPNSMRMSLVRHLLSDPSGAVMVRAYLER : 529
AdonisE2     : SMQAWSSLWPKERKRQRAFFLFGLELIVQLDIEATRTFFRTFFRLPTWMWWGFLGSSLSSFDLVLFSMYMFVLAPNSMRMSLVRHLLSDPSGAVMVKAYLER : 529
LettuceEE    : SKQAWETLWPLERKRQRAFFLFGLSHIVLMDLEGTRTFFRTFFRLPKWMWWGFLGSSLSSTDLIIFALYMFVIAPHSLRMELVRHLLSDPTGATMVKAYLTI : 533
TomatoE      : STQAWNTLWPQERKRQRSFFLFGLALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSSADLMLFAFYMFIIAPNDMRKGLIRHLLSDPTGATLIRTYLTF : 526
MarigoldE    : SKQAWETLWPLERKRQRAFFLFGLALIVQMDIEGTRTFFRTFFRLPTWMWWGFLGSSLSSTDLIIFAFYMFIIAPHSLRMGLVRHLLSDPTGGTMLKAYLTI : 516
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FIG. 26B

FIG. 25C

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                      *     460       *      480       *      500       *      520       *      540       *
PotatoE      : STPS-ISTQAWNTLWPQERKRQRSFFLFGLALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSXADLMLFAFYMFIIAPNDMRRGLIRHLLSDPTGATLIRTYLTF-- : 378
ArabidopsisE : ----NISRQAWDTLWPPERKRQRAFFLFGLALIVQFDTEGIRSFFRTFFRLPKWMWQGFLGSTLTSGDLVLFALYMFVISPNNLRKGLINHLISDPTGATMIKTYLKV-- : 524
AdonisE1     : SSAVNISMQAWSSLWPKERKRQRAFFLFGLELIVQLDIEATRTFFRTFFRLPTWMWGFLGSSLSSFDLVLFSMYMFVLAPNSMRMSLVRHLLSDPSGAVMVRAYLER-- : 529
AdonisE1     : SSAVNISMQAWSSLWPKERKRQRAFFLFGLELIVQLDIEATRTFFRTFFRLPTWMWGFLGSSLSSFDLVLFSMYMFVLAPNSMRMSLVRHLLSDPSGAVMVKAYLER-- : 529
LettuceEE    : KYT-NISKQAWETLWPLERKRQRAFFLFGLSHIVLMDLEGTRTFFRTFFRLPKWMWGFLGSSLSSTDLIIFALYMFVIAPHSLRMELVRHLLSDPTGATMVKAYLTI-- : 533
TomatoE      : SSIPSISTQAWNTLWPQERKRQRSFFLFGLALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSSADLMLFAFYMFIIAPNDMRKGLIRHLLSDPTGATLIRTYLTF-- : 526
MarigoldE    : RYTTNISKQAWETLWPLERKRQRAFFLFGLALIVQMDIEGTRTFFRTFFRLPTWMWGFLGSSLSSTDLIIFAFYMFIIAPHSLRMGLVRHLLSDPTGGTMLKAYLTI-- : 516
ArabidopsisB : LRGDQLSAEVWRDLWPIERRRQREFFCFGMDILLKLDLDATRRFFDAFFDLQPHYWHGFLSSRLFLPELLVFGLSLFSHASNTSRLEIMTK-GTVP-LAKMINNLVQDRD : 501
AdonisB      : -SGNELSAEVWKDLWPIERRRQREFFCFGMDILLKLDLQGTRRFFDAFFDLEPHYWHGFLSSRLFLPELLFFGLSLFSHASNASRIEIMAK-GTVP-LVNMMNNLIPDTD : 502
PepperB      : -SGDELSAAVWKDLWRIERRRQREFFCFGMDILLKLDLPATRRFFDAFFDLEPRYWHGFLSSRLFLPELIVFGLSLFSHASNTSRLEIMTK-GTLP-LVHMINNLLQDKE : 498
TomatoB      : -SGNELSTAVWKDLWPIERRRQREFFCFGMDILLKLDLPATRRFFDAFFDLEPRYWHGFLSSRLFLPELIVFGLSLFSHASNTSRFEIMTK-GTVP-LVNMINNLLQDKE : 500
TobaccoB     : -LGNELSAAVWKDLWPIERRRQREFFCFGMDILLKLDLPATRRFFDAFFDLEPRYWHGFLSSRLYLPELIFFGLSLFSRASNTSRIEIMTK-GTLP-LVNMINNLLQDTE : 500
MarigoldB    : VTGDDLAAGIWRELWPIERRRQREFFCFGMDILLKLDLEGTRRFFDAFFDLEPRYWHGFLSSRLFLPELVTFGLSLFGHASNTCRVEIMAK-GTLP-LATMIGNLVRDRE : 511
DaffodilB    : -SGNDLSADVWKDLWPIERRRQREFFCFGMDILLKLDLEGTRRFFDAFFDLEPRYWHGFLSSRLFLPELVPFGLSLFSHASNTCKLEIMAK-GTLP-LVNMINNLVQDRD : 503
```

FIG. 26A

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                      *        20         *        40         *        60         *        80         *       100         *
PotatoE      : ------------------------------------------------------------------------------------------------------------ : -
ArabidopsisE : MECVGARNF-AAMAVSTFPSWS-CRRKFPVVKRYSYRNIRFGL-CSV--RASGGGSSGSESCVAVREDF--ADEEDFVKAGGSEILFVQMQQNKDMDEQSKLVDKLPPIS : 103
AdonisE1     : MELLGVRNL-----ISSCPVMT-FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGSRSSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPIP : 102
AdonisE2     : MELLGVRNL-----ISSCPVWT-FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGSRTSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPIP : 102
LettuceEE    : MECFGARNMTATMAVFTCPRFTDCNIRHKFSLLKQRRFTNLSA-SSSLRQIKCSAKSDR--CVVDKQGISVADEEDYVKAGGSELFFVQMQRTKSMESQSKLSEKLAQIP : 107
TomatoE      : MECVGVQNV-GAMAVLTRPRLN----RWSGGELCQEKSIFLAY-EQY--ESKCNSSSGSDSCVVDKEDF--ADEEDYIKAGGSQLVFVQMQQKKDMDQQSKLSDELRQIS : 100
MarigoldE    : MSMRAG-HMTATMAAFTCPRFM--------------TSIRYT------KQIKCNAAKSQ---LVVKQEI--EEEEDYVKAGGSELLFVQMQQNKSMDAQSSLSQKLPRVP :  84

                    120         *       140         *       160         *       180         *       200         *       220
PotatoE      : ---------------------------------------------------------DEFKDLGLQACIEHVWRDTIVYLDDDDPILIGRAYGRVSRHLLHEELKRCVEAGVL :  57
ArabidopsisE : IG-----DGALDHVVIGCGPAGLALAAESAKLGLKVGLIGPDLPFTNNYGVWEDEFNDLGLQKCIEHVWRETIVYLDDDKPITIGRAYGRVSRRLLHEELLRRCVESGVS : 208
AdonisE1     : FG-----ESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWEDEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKRCVESGVS : 207
AdonisE2     : FG-----ESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWEDEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKRCVESGVS : 207
LettuceEE    : IG-----NCILDLVVIGCGPAGLALAAESAKLGLNVGLIGPDLPFTNNYGVWQDEFIGLGLEGCIEHSWKDTLVYLDDADPIRIGRAYGRVHRDLLHEELLRRCVESGVS : 212
TomatoE      : AG-----QTVLDLVVIGCGPAGLALAAESAKLGLNVGLVGPDLPFTNNYGVWEDEFKDLGLQACIEHVWRDTIVYLDDDEPILIGRAYGRVSRHFLHEELLKRCVEAGVL : 205
MarigoldE    : IGGGGDSNCILDLVVIGCGPAGLALAGESAKLGLNVALIGPDLPFTNNYGVWEDEFIGLGLEGCIEHVWRDTVVYLDDNDPILIGRAYGRVSRDLLHEELLTRCMESGVS : 194
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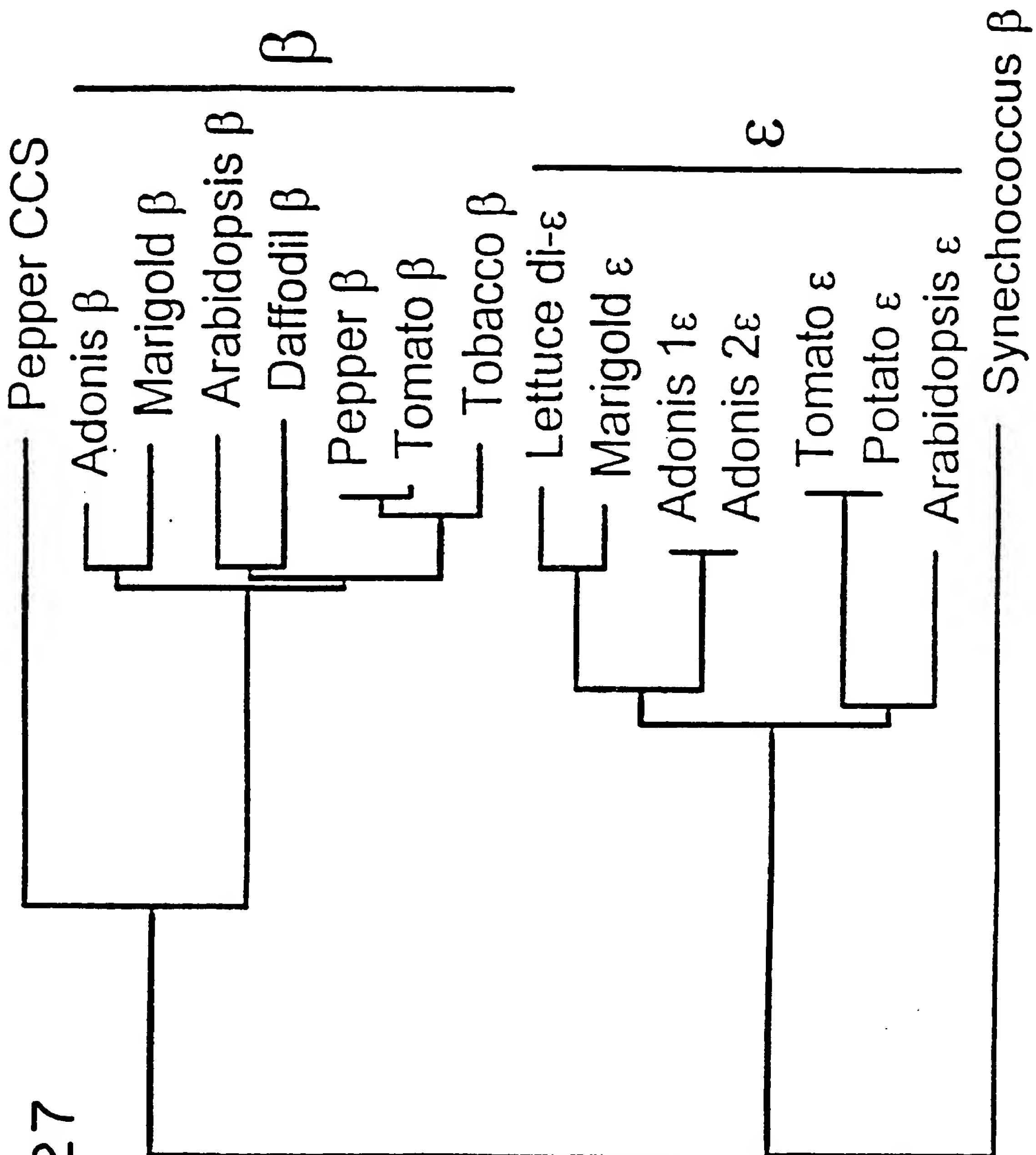
β
ε
Pepper CCS
Adonis β
Marigold β
Arabidopsis β
Daffodil β
Pepper β
Tomato β
Tobacco β
Lettuce di-ε
Marigold ε
Adonis 1ε
Adonis 2ε
Tomato ε
Potato ε
Arabidopsis ε
Synechococcus β

FIG. 27

FIG. 28A

```
GAP of:  Arabidopsis epsilon cyclase to Lettuce epsilon cyclase
           Gap Weight:     12          Average Match:   2.912
        Length Weight:      4       Average Mismatch:  -2.003
              Quality:   1837                 Length:     534
                Ratio:  3.499                   Gaps:       3
   Percent Similarity: 76.381       Percent Identity:  69.905
Match display thresholds for the alignment(s):
                | = IDENTITY    : = 2    . = 1

Arabidopsis x Lettuce
                   .         .         .         .         .
     1 MECVGARNF.AAMAVSTFFPSW...SCRRKFPVVKRYSYRNIRFGLCSVRA 46
       ||| ||||  | ||| | | .   . | ||  ..|.  : |:      .
     1 MECFGARNMTATMAVFTCPRFTDCNIRHKFSLLKQRRFTNLSASSSLRQI 50
                   .         .         .         .         .
    47 SGGGSSGSESCVAVREDFADEEDFVKAGGSEILFVQMQQNKDMDEQSKLV 96
            |              |||||:|||||||: |||||. | |: ||||
    51 KCSAKSDRCVVDKQGISVADEEDYVKAGGSELFFVQMQRTKSMESQSKLS 100
                   .         .         .         .         .
    97 DKLPPISIGDGALDHVVIGCGPAGLALAAESAKLGLKVGLIGPDLPFTNN 146
       :||   | ||.  || ||||||||||||||||||||| ||||||||||||
   101 EKLAQIPIGNCILDLVVIGCGPAGLALAAESAKLGLNVGLIGPDLPFTNN 150
                   .         .         .
   147 YGVWEDEFNDLGLQKCIEHVWRETIVYLDDDKPITIGRAYGRVSRRLLHE 196
       ||||:|||  |||: |||| |::|:|||||  || |||||||| | ||||
   151 YGVWQDEFIGLGLEGCIEHSWKDTLVYLDDADPIRIGRAYGRVHRDLLHE 200
                   .         .         .         .         .
   197 ELLRRCVESGVSYLSSKVDSITEASDGLRLVACDDNNAIPCRLATVASGA 246
       ||||||||||||||||||: |||| .|   |: |: |   ||||||||||||
   201 ELLRRCVESGVSYLSSKVERITEAPNGYSLIECEGNITIPCRLATVASGA 250
                   .         .         .         .         .
   247 ASGKLLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVFMDYRDYTNEKV 296
       |||| |:||.||||||||||||:||||||.||||| ||||||||:.   |
   251 ASGKFLEYELGGPRVCVQTAYGIEVEVENNPYDPDLMVFMDYRDFSKHKP 300
                   .         .         .         .         .
   297 RSLEAEYPTFLYAMPMTKSRLFFEETCLASKDVMPFDLLKTKLMLRLDTL 346
        ||||.|||||| | |. .::|||||||||:: |||.|||.||| ||   :
   301 ESLEAKYPTFLYVMAMSPTKIFFEETCLASREAMPFNLLKSKLMSRLKAM 350
```

FIG. 28B

```
             .         .         .         .         .
347 GIRILKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSL 396
    |||| :||||||||||||||||||||||||||||||||||||||||||||
351 GIRITRTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSL 400

             .         .         .         .         .
397 SEAPKYASVIAEILREETTKQINS.....NISRQAWDTLWPPERKRQRAF 441
    |||| ||.|||.|||:: .|:. |     |||:|||:|||| ||||||||
401 SEAPNYAAVIAKILRQDQSKEMISLGKYTNISKQAWETLWPLERKRQRAF 450

             .         .         .         .         .
442 FLFGLALIVQFDTEGIRSFFRTFFRLPKWMWQGFLGSTLTSGDLVLFALY 491
    |||||. ||  | || |.||||||||||||| |||||.|.| ||::||||
451 FLFGLSHIVLXDLEGTRTFFRTFFRLPKWMWWGFLGSSLSSTDLIIFALY 500

             .         .         .
492 MFVISPNNLRKGLINHLISDPTGATMIKTYLKV* 525
    ||||.|..||  |: ||:||||||||:| || :|
501 MFVIAPHSLRMELVRHLLSDPTGATMVKAYLTI* 534
```

SEQUENCE LISTING

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<110> CUNNINGHAM JR., FRANCIS X.
      SUN, ZAIREN

<120> GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
      METHODS OF USE THEREOF

<130> 8172-9023

<140> NOT YET ASSIGNED
<141> 1999-06-02

<150> 09/088,724
<151> 1998-06-02

<150> 09/088,725
<151> 1998-06-02

<160> 61

<170> PatentIn Ver. 2.0

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                                                     Met Glu Cys
                                                       1

GTT GGG GCT AGG AAT TTC GCA GCA ATG GCG GTT TCA ACA TTT CCG TCA     165
Val Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr Phe Pro Ser
      5                  10                  15

TGG AGT TGT CGA AGG AAA TTT CCA GTG GTT AAG AGA TAC AGC TAT AGG     213
Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr Ser Tyr Arg
 20                  25                  30                  35

AAT ATT CGT TTC GGT TTG TGT AGT GTC AGA GCT AGC GGC GGC GGA AGT     261
Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly Gly Gly Ser
                 40                  45                  50

TCC GGT AGT GAG AGT TGT GTA GCG GTG AGA GAA GAT TTC GCT GAC GAA     309
Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe Ala Asp Glu
             55                  60                  65

GAA GAT TTT GTG AAA GCT GGT GGT TCT GAG ATT CTA TTT GTT CAA ATG     357
Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe Val Gln Met
         70                  75                  80

CAG CAG AAC AAA GAT ATG GAT GAA CAG TCT AAG CTT GTT GAT AAG TTG     405
```

```
Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val Asp Lys Leu
     85                  90                  95

CCT CCT ATA TCA ATT GGT GAT GGT GCT TTG GAT CAT GTG GTT ATT GGT      453
Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val Val Ile Gly
100                 105                 110                 115

TGT GGT CCT GCT GGT TTA GCC TTG GCT GCA GAA TCA GCT AAG CTT GGA      501
Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly
                120                 125                 130

TTA AAA GTT GGA CTC ATT GGT CCA GAT CTT CCT TTT ACT AAC AAT TAC      549
Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr
            135                 140                 145

GGT GTT TGG GAA GAT GAA TTC AAT GAT CTT GGG CTG CAA AAA TGT ATT      597
Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln Lys Cys Ile
        150                 155                 160

GAG CAT GTT TGG AGA GAG ACT ATT GTG TAT CTG GAT GAT GAC AAG CCT      645
Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp Asp Lys Pro
    165                 170                 175

ATT ACC ATT GGC CGT GCT TAT GGA AGA GTT AGT CGA CGT TTG CTC CAT      693
Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg Leu Leu His
180                 185                 190                 195

GAG GAG CTT TTG AGG AGG TGT GTC GAG TCA GGT GTC TCG TAC CTT AGC      741
Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser
                200                 205                 210

TCG AAA GTT GAC AGC ATA ACA GAA GCT TCT GAT GGC CTT AGA CTT GTT      789
Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu Arg Leu Val
            215                 220                 225

GCT TGT GAC GAC AAT AAC GTC ATT CCC TGC AGG CTT GCC ACT GTT GCT      837
Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala Thr Val Ala
        230                 235                 240

TCT GGA GCA GCT TCG GGA AAG CTC TTG CAA TAC GAA GTT GGT GGA CCT      885
Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly Pro
    245                 250                 255

AGA GTC TGT GTG CAA ACT GCA TAC GGC GTG GAG GTT GAG GTG GAA AAT      933
Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn
260                 265                 270                 275

AGT CCA TAT GAT CCA GAT CAA ATG GTT TTC ATG GAT TAC AGA GAT TAT      981
Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr Arg Asp Tyr
                280                 285                 290

ACT AAC GAG AAA GTT CGG AGC TTA GAA GCT GAG TAT CCA ACG TTT CTG     1029
Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro Thr Phe Leu
            295                 300                 305

TAC GCC ATG CCT ATG ACA AAG TCA AGA CTC TTC TTC GAG GAG ACA TGT     1077
Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu Glu Thr Cys
        310                 315                 320

TTG GCC TCA AAA GAT GTC ATG CCC TTT GAT TTG CTA AAA ACG AAG CTC     1125
Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys Thr Lys Leu
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    325                 330                 335

ATG TTA AGA TTA GAT ACA CTC GGA ATT CGA ATT CTA AAG ACT TAC GAA       1173
Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys Thr Tyr Glu
340                 345                 350                 355

GAG GAG TGG TCC TAT ATC CCA GTT GGT GGT TCC TTG CCA AAC ACC GAA       1221
Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu
                360                 365                 370

CAA AAG AAT CTC GCC TTT GGT GCT GCC GCT AGC ATG GTA CAT CCC GCA       1269
Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala
            375                 380                 385

ACA GGC TAT TCA GTT GTG AGA TCT TTG TCT GAA GCT CCA AAA TAT GCA       1317
Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Tyr Ala
        390                 395                 400

TCA GTC ATC GCA GAG ATA CTA AGA GAA GAG ACT ACC AAA CAG ATC AAC       1365
Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys Gln Ile Asn
    405                 410                 415

AGT AAT ATT TCA AGA CAA GCT TGG GAT ACT TTA TGG CCA CCA GAA AGG       1413
Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro Pro Glu Arg
420                 425                 430                 435

AAA AGA CAG AGA GCA TTC TTT CTC TTT GGT CTT GCA CTC ATA GTT CAA       1461
Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln
                440                 445                 450

TTC GAT ACC GAA GGC ATT AGA AGC TTC TTC CGT ACT TTC TTC CGC CTT       1509
Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe Phe Arg Leu
            455                 460                 465

CCA AAA TGG ATG TGG CAA GGG TTT CTA GGA TCA ACA TTA ACA TCA GGA       1557
Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu Thr Ser Gly
        470                 475                 480

GAT CTC GTT CTC TTT GCT TTA TAC ATG TTC GTC ATT TCA CCA AAC AAT       1605
Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser Pro Asn Asn
    485                 490                 495

TTG AGA AAA GGT CTC ATC AAT CAT CTC ATC TCT GAT CCA ACC GGA GCA       1653
Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro Thr Gly Ala
500                 505                 510                 515

ACC ATG ATA AAA ACC TAT CTC AAA GTA TGATTTACTT ATCAACTCTT            1700
Thr Met Ile Lys Thr Tyr Leu Lys Val
                520

AGGTTTGTGT ATATATATGT TGATTTATCT GAATAATCGA TCAAAGAATG GTATGTGGGT    1760

TACTAGGAAG TTGGAAACAA ACATGTATAG AATCTAAGGA GTGATCGAAA TGGAGATGGA    1820

AACGAAAAGA AAAAAATCAG TCTTTGTTTT GTGGTTAGTG                          1860
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<400> 2

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Ser Tyr Arg Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly
35 40 45

Gly Gly Ser Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe
50 55 60

Ala Asp Glu Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe
65 70 75 80

Val Gln Met Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val
85 90 95

Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val
100 105 110

Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala
115 120 125

Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
130 135 140

Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
145 150 155 160

Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp
165 170 175

Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg
180 185 190

Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
195 200 205

Tyr Leu Ser Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu
210 215 220

Arg Leu Val Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala
225 230 235 240

Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val
245 250 255

Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu
260 265 270

Val Glu Asn Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr
275 280 285

Arg Asp Tyr Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro
290 295 300

Thr Phe Leu Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu
305 310 315 320

Glu Thr Cys Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys
325 330 335

Thr Lys Leu Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys
340 345 350

Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro
355 360 365

Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val
370 375 380

His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro
385 390 395 400

Lys Tyr Ala Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys
405 410 415

Gln Ile Asn Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro
420 425 430

Pro Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu
435 440 445

Ile Val Gln Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe
450 455 460

Phe Arg Leu Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu
465 470 475 480

Thr Ser Gly Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser
485 490 495

Pro Asn Asn Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro
500 505 510

Thr Gly Ala Thr Met Ile Lys Thr Tyr Leu Lys Val
515 520

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<213> Arabidopsis thaliana

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AGAATTCTCC GATTGAGAAC GATGAGAGAC CGGAGAGCAC GAGCTCCACA AACGCTATAG 180

ACGCTGAGTA TCTGGCGTTG CGTTTGGCGG AGAAATTGGA GAGGAAGAAA TCGGAGAGGT 240

CCACTTATCT AATCGCTGCT ATGTTGTCGA GCTTTGGTAT CACTTCTATG GCTGTTATGG 300

CTGTTTACTA CAGATTCTCT TGGCAAATGG AGGGAGGTGA GATCTCAATG TTGGAAATGT 360

TTGGTACATT TGCTCTCTCT GTTGGTGCTG CTGTTGGTAT GGAATTCTGG GCAAGATGGG 420

CTCATAGAGC TCTGTGGCAC GCTTCTCTAT GGAATATGCA TGAGTCACAT CACAAACCAA 480

GAGAAGGACC GTTTGAGCTA AACGATGTTT TTGCTATAGT GAACGCTGGT CCAGCGATTG 540

GTCTCCTCTC TTATGGATTC TTCAATAAAG GACTCGTTCC TGGTCTCTGC TTTGGCGCCG 600

GGTTAGGCAT AACGGTGTTT GGAATCGCCT ACATGTTTGT CCACGATGGT CTCGTGCACA 660

AGCGTTTCCC TGTAGGTCCC ATCGCCGACG TCCCTTACCT CCGAAAGGTC GCCGCCGCTC 720

ACCAGCTACA TCACACAGAC AAGTTCAATG GTGTACCATA TGGACTGTTT CTTGGACCCA 780

AGGAATTGGA AGAAGTTGGA GGAAATGAAG AGTTAGATAA GGAGATTAGT CGGAGAATCA 840

AATCATACAA AAAGGCCTCG GGCTCCGGGT CGAGTTCGAG TTCTTGACTT TAAACAAGTT 900

TTAAATCCCA AATTCTTTTT TTGTCTTCTG TCATTATGAT CATCTTAAGA CGGTCT 956

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<213> Arabidopsis thaliana

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Tyr Val Val Glu Glu Arg Arg Gln Asn Ser Pro Ile Glu Asn Asp Glu
35 40 45

Arg Pro Glu Ser Thr Ser Ser Thr Asn Ala Ile Asp Ala Glu Tyr Leu
50 55 60

Ala Leu Arg Leu Ala Glu Lys Leu Glu Arg Lys Lys Ser Glu Arg Ser
65 70 75 80

Thr Tyr Leu Ile Ala Ala Met Leu Ser Ser Phe Gly Ile Thr Ser Met
85 90 95

Ala Val Met Ala Val Tyr Tyr Arg Phe Ser Trp Gln Met Glu Gly Gly
100 105 110

Glu Ile Ser Met Leu Glu Met Phe Gly Thr Phe Ala Leu Ser Val Gly
115 120 125

Ala Ala Val Gly Met Glu Phe Trp Ala Arg Trp Ala His Arg Ala Leu
130 135 140

Trp His Ala Ser Leu Trp Met Asn His Glu Ser His His Lys Pro Arg
145 150 155 160

Glu Gly Pro Phe Glu Leu Asn Asp Val Phe Ala Ile Val Asn Ala Gly
165 170 175

Pro Ala Ile Gly Leu Leu Ser Tyr Gly Phe Phe Asn Lys Gly Leu Val
180 185 190

Pro Gly Leu Cys Phe Gly Ala Gly Leu Gly Ile Thr Val Phe Gly Ile
195 200 205

Ala Tyr Met Phe Val His Asp Gly Leu Val His Lys Arg Phe Pro Val
210 215 220

Gly Pro Ile Ala Asp Val Pro Tyr Leu Arg Lys Val Ala Ala Ala His
225 230 235 240

Gln Leu His His Thr Asp Lys Phe Asn Gly Val Pro Tyr Gly Leu Phe
245 250 255

Leu Gly Pro Lys Glu Leu Glu Glu Val Gly Gly Asn Glu Glu Leu Asp
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Lys Glu Ile Ser Arg Arg Ile Lys Ser Tyr Lys Lys Ala Ser Gly Ser
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Gly Ser Ser Ser Ser Ser
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<213> Alicalgenes sp.

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20 25 30

Gly Trp His Lys Ser His His Glu Glu His Asp His Ala Leu Glu Lys
35 40 45

Asn Asp Leu Tyr Gly Val Val Phe Ala Val Leu Ala Thr Ile Leu Phe
50 55 60

Thr Val Gly Ala Tyr Trp Trp Pro Val Leu Trp Trp Ile Ala Leu Gly
65 70 75 80

Met Thr Val Tyr Gly Leu Ile Tyr Phe Ile Leu His Asp Gly Leu Val
85 90 95

His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Arg Gly Tyr Phe Arg
100 105 110

Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
115 120 125

His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
130 135 140

Lys Gln Asp Leu Lys Arg Ser Gly Val Leu Arg Pro Gln Asp Glu Arg
145 150 155 160

Pro Ser

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<211> 175
<212> PRT
<213> Erwinia herbicola

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20 25 30

Trp His Glu Ser His His Thr Pro Arg Lys Gly Val Phe Glu Leu Asn
35 40 45

Asp Leu Phe Ala Val Val Phe Ala Gly Val Ala Ile Ala Leu Ile Ala
50 55 60

Val Gly Thr Ala Gly Val Trp Pro Leu Gln Trp Ile Gly Cys Gly Met
65 70 75 80

Thr Val Tyr Gly Leu Leu Tyr Phe Leu Val His Asp Gly Leu Val His
85 90 95

Gln Arg Trp Pro Phe His Trp Ile Pro Arg Arg Gly Tyr Leu Lys Arg
100 105 110

Leu Tyr Val Ala His Arg Leu His His Ala Val Arg Gly Arg Glu Gly
115 120 125

Cys Val Ser Phe Gly Phe Ile Tyr Ala Arg Lys Pro Ala Asp Leu Gln
130 135 140

Ala Ile Leu Arg Glu Arg His Gly Arg Pro Pro Lys Arg Asp Ala Ala
145 150 155 160

Lys Asp Arg Pro Asp Ala Ala Ser Pro Ser Ser Ser Ser Pro Glu
165 170 175

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<212> PRT
<213> Erwinia uredovora

<400> 7
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20 25 30

Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu
50 55 60

Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
65 70 75 80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
100 105 110

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Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
        115                 120                 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
    130                 135                 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala
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Ala Arg Asp Ala Gln Gly Gly Glu Asp Glu Pro Ala Ser Gly Lys
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<213> Agrobacterium aurianticum

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             20                  25                  30

Gly Trp His Lys Ser His His Glu Glu His Asp His Ala Leu Glu Lys
         35                  40                  45

Asn Asp Leu Tyr Gly Leu Val Phe Ala Val Ile Ala Thr Val Leu Phe
     50                  55                  60

Thr Val Gly Trp Ile Trp Ala Pro Val Leu Trp Trp Ile Ala Leu Gly
 65                  70                  75                  80

Met Thr Val Tyr Gly Leu Ile Tyr Phe Val Leu His Asp Gly Leu Val
                 85                  90                  95

His Trp Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr Ala Arg
            100                 105                 110

Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
        115                 120                 125

His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
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Lys Gln Asp Leu Lys Met Ser Gly Val Leu Arg Ala Glu Ala Gln Glu
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<212> DNA
<213> Arabidopsis thaliana

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TTCAGAGACG ACTCATGTTT GAAGACGAAT GCATTCTCGT TGATGAAAAT AATCGTGTGG 180

TGGGACATGA CACTAAGTAT AACTGTCATC TGATGGAAAA GATTGAAGCT GAGAATTTAC 240

TTCACAGAGC TTTCAGTGTG TTTTTATTCA ACTCCAAGTA TGAGTTGCTT CTCCAGCAAC 300

GGTCAAAAAC AAAGGTTACT TTCCCACTTG TGTGGACAAA CACTTGTTGC AGCCATCCTC 360

TTTACCGTGA ATCCGAGCTT ATTGAAGAGA ATGTGCTTGG TGTAAGAAAT GCCGCACAAA 420

GGAAGCTTTT CGATGAGCTC GGTATTGTAG CAGAAGATGT ACCAGTCGAT GAGTTCACTC 480

CCTTGGGACG CATGCTTTAC AAGGCACCTT CTGATGGGAA ATGGGGAGAG CACGAAGTTG 540

ACTATCTACT CTTCATCGTG CGGGATGTGA AGCTTCAACC AAACCCAGAT GAAGTGGCTG 600

AGATCAAGTA CGTGAGCAGG GAAGAGCTTA AGGAGCTGGT GAAGAAAGCA GATGCTGGCG 660

ATGAAGCTGT GAAACTATCT CCATGGTTCA GATTGGTGGT GGATAATTTC TTGATGAAGT 720

GGTGGGATCA TGTTGAGAAA GGAACTATCA CTGAAGCTGC AGACATGAAA ACCATTCACA 780

AGCTCTGAAC TTTCCATAAG TTTTGGATCT TCCCCTTCCC ATAATAAAAT TAAGAGATGA 840

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TTTTTATTTA CTTTTGATTC ATCTCTAGTT TAGTTTTCAT CTTAAAAAAA AAAA 954

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<212> DNA
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GAAAGTTACC GAATTTTCGT GCTTTCTCTG GTACCGCTAT GACAGATACT AAAGATGCTG 180

GTATGGATGC TGTTCAGAGA CGTCTCATGT TTGAGGATGA ATGCATTCTT GTTGATGAAA 240

CTGATCGTGT TGTGGGGCAT GTCAGCAAGT ATAATTGTCA TCTGATGGAA AATATTGAAG 300

CCAAGAATTT GCTGCACAGG GCTTTTAGTG TATTTTTATT CAACTCGAAG TATGAGTTGC 360

TTCTCCAGCA AAGGTCAAAC ACAAAGGTTA CGTTCCCTCT AGTGTGGACT AACACTTGTT 420

GCAGCCATCC TCTTTACCGT GAATCAGAGC TTATCCAGGA CAATGCACTA GGTGTGAGGA 480

ATGCTGCACA AAGAAAGCTT CTCGATGAGC TTGGTATTGT AGCTGAAGAT GTACCAGTCG 540

ATGAGTTCAC TCCCTTGGGA CGTATGCTGT ACAAGGCTCC TTCTGATGGC AAATGGGGAG 600

AGCATGAACT TGATTACTTG CTCTTCATCG TGCGAGACGT GAAGGTTCAA CCAAACCCAG 660

ATGAAGTAGC TGAGATCAAG TATGTGAGCC GGGAAGAGCT GAAGGAGCTG GTGAAGAAAG 720

CAGATGCAGG TGAGGAAGGT TTGAAACTGT CACCATGGTT CAGATTGGTG GTGGACAATT 780

TCTTGATGAA GTGGTGGGAT CATGTTGAGA AAGGAACTTT GGTTGAAGCT ATAGACATGA 840

AAACCATCCA CAAACTCTGA ACATCTTTTT TTAAAGTTTT TAAATCAATC AACTTTCTCT 900

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CCAAGCACCT CAGGCAATAA TAAAGTTTGC GGCCGC 996

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<212> DNA
<213> Haematococcus pluvialis

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CAAGCACCTG GGCAGGCGGG CAGTCGCAGG ATGAGCTGAT GCTGAAGGAC GAGTGCATCT 300

TGGTGGATGT TGAGGACAAC ATCACAGGCC ATGCCAGCAA GCTGGAGTGT CACAAGTTCC 360

TACCACATCA GCCTGCAGGC CTGCTGCACC GGGCCTTCTC TGTGTTCCTG TTTGACGATC 420

AGGGGCGACT GCTGCTGCAA CAGCGTGCAC GCTCAAAAAT CACCTTCCCA AGTGTGTGGA 480

CGAACACCTG CTGCAGCCAC CCTTTACATG GGCAGACCCC AGATGAGGTG GACCAACTAA 540

GCCAGGTGGC CGACGGAACA GTACCTGGCG CAAAGGCTGC TGCCATCCGC AAGTTGGAGC 600

ACGAGCTGGG GATACCAGCG CACCAGCTGC CGGCAAGCGC GTTTCGCTTC CTCACGCGTT 660

TGCACTACTG TGCCGCGGAC GTGCAGCCAG CTGCGACACA ATCAGCGCTC TGGGGCGAGC 720

ACGAAATGGA CTACATCTTG TTCATCCGGG CCAACGTCAC CTTGGCGCCC AACCCTGACG 780

AGGTGGACGA AGTCAGGTAC GTGACGCAAG AGGAGCTGCG GCAGATGATG CAGCCGGACA 840

ACGGGCTGCA ATGGTCGCCG TGGTTTCGCA TCATCGCCGC GCGCTTCCTT GAGCGTTGGT 900

GGGCTGACCT GGACGCGGCC CTAAACACTG ACAAACACGA GGATTGGGGA ACGGTGCATC 960

ACATCAACGA AGCGTGAAAG CAGAAGCTGC AGGATGTGAA GACACGTCAT GGGGTGGAAT 1020

TGCGTACTTG GCAGCTTCGT ATCTCCTTTT TCTGAGACTG AACCTGCAGT CAGGTCCCAC 1080

AAGGTCAGGT AAAATGGCTC GATAAAATGT ACCGTCACTT TTTGTCGCGT ATACTGAACT 1140

CCAAGAGGTC AAAAAAAAAA AAAAA 1165

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<213> Haematococcus pluvialis

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CCAGCTGTGC ACACGCGCGA CTCCAGTTTA AGCTCAGGAG CATGCAGCTG CTTTCCGAGG 180

ACCGCACAGA CCACATGAGG GGTGCAAGCA CCTGGGCAGG CGGGCAGTCG CAGGATGAGC 240

TGATGCTGAA GGACGAGTGC ATCTTGGTAG ATGTTGAGGA CAACATCACA GGCCATGCCA 300

GCAAGCTGGA GTGTCACAAG TTCCTACCAC ATCAGCCTGC AGGCCTGCTG CACCGGGCCT 360

TCTCTGTGTT CCTGTTTGAC GATCAGGGGC GACTGCTGCT GCAACAGCGT GCACGCTCAA 420

AAATCACCTT CCCAAGTGTG TGGACGAACA CCTGCTGCAG CCACCCTTTA CATGGGCAGA 480

CCCCAGATGA GGTGGACCAA CTAAGCCAGG TGGCCGACGG AACAGTACCT GGCGCAAAGG 540

CTGCTGCCAT CCGCAAGTTG GAGCACGAGC TGGGGATACC AGCGCACCAG CTGCCGGCAA 600

GCGCGTTTCG CTTCCTCACG CGTTTGCACT ACTGTGCCGC GGACGTGCAG CCAGCTGCGA 660

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TCACCTTGGC GCCCAACCCT GACGAGGTGG ACGAAGTCAG GTACGTGACG CAAGAGGAGC 780

TGCGGCAGAT GATGCAGCCG GACAACGGGC TTCAATGGTC GCCGTGGTTT CGCATCATCG 840

CCGCGCGCTT CCTTGAGCGT TGGTGGGCTG ACCTGGACGC GGCCCTAAAC ACTGACAAAC 900

ACGAGGATTG GGGAACGGTG CATCACATCA ACGAAGCGTG AAGGCAGAAG CTGCAGGATG 960

TGAAGACACG TCATGGGGTG GAATTGCGTA CTTGGCAGCT TCGTATCTCC TTTTTCTGAG 1020

ACTGAACCTG CAGAGCTAGA GTCAATGGTG CATCATATTC ATCGTCTCTC TTTTGTTTTA 1080

GACTAATCTG TAGCTAGAGT CACTGATGAA TCCTTTACAA CTTTCAAAAA AAAAA 1135

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GTAAAATGCT GCACAGAGCA TTCAGCGTTT TTCTATTCAA TTCAAAATAC GAGTTACTTC 240

TTCAGCAACG GTCTGCAACC AAGGTGACAT TTCCTTTAGT ATGGACCAAC ACCTGTTGCA 300

GCCATCCACT CTACAGAGAA TCCGAGCTTG TTCCCGAAAC GCCTGAGAGA ATGCTGCACA 360

GAGGANNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 420

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NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 660

NNNNNNNNNN NNNNNNNNNN TCATGTGCAA AAGGGTACAC TCACTGAATG CAATTTGATA 720

TGAAAACCAT ACACAAGCTG ATATAGAAAC ACACCCTCAA CCGAAAAGCA AGCCTAATAA 780

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TTTGAGCATG TTGATTCTTG TCTTTTGTGT GTAAGATTTT GGGTTTCGTT TCAGTTGTAA 900

TAATGAACCA TTGATGGTTT GCAATTTCAA GTTCCTATCG ACATGTAGTG ATCTAAAAAA 960

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<212> PRT
<213> Haematococcus pluvialis

<400> 14
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35 40 45

Ser Arg Ala Glu Asp Arg Thr Asp His Met Arg Gly Ala Ser Thr Trp
50 55 60

Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys Asp Glu Cys Ile
65 70 75 80

Leu Val Asp Val Glu Asp Asn Ile Thr Gly His Ala Ser Lys Leu Glu
85 90 95

Cys His Lys Phe Leu Pro His Gln Pro Ala Gly Leu Leu His Arg Ala
100 105 110

Phe Ser Val Phe Leu Phe Asp Asp Gln Gly Arg Leu Leu Leu Gln Gln
115 120 125

Arg Ala Arg Ser Lys Ile Thr Phe Pro Ser Val Trp Thr Asn Thr Cys
130 135 140

Cys Ser His Pro Leu His Gly Gln Thr Pro Asp Glu Val Asp Gln Leu
145 150 155 160

Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys Ala Ala Ala Ile
165 170 175

Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His Gln Leu Pro Ala
180 185 190

Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys Ala Ala Asp Val
195 200 205

Gln Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu His Glu Met Asp
210 215 220

Tyr Ile Leu Phe Ile Arg Ala Asn Val Thr Leu Ala Pro Asn Pro Asp
225 230 235 240

Glu Val Asp Glu Val Arg Tyr Val Thr Gln Glu Glu Leu Arg Gln Met
245 250 255

Met Gln Pro Asp Asn Gly Leu Gln Trp Ser Pro Trp Phe Arg Ile Ile
260 265 270

Ala Ala Arg Phe Leu Glu Arg Trp Trp Ala Asp Leu Asp Ala Ala Leu
275 280 285

Asn Thr Asp Lys His Glu Asp Trp Gly Thr Val His His Ile Asn Glu
290 295 300

Ala
305

<210> 15
<211> 293
<212> PRT
<213> Haematococcus pluvialis

<400> 15
Met Leu Arg Ser Leu Leu Arg Gly Leu Thr His Ile Pro Arg Val Asn
1 5 10 15

Ser Ala Gln Gln Pro Ser Cys Ala His Ala Arg Leu Gln Phe Lys Leu
20 25 30

Arg Ser Met Gln Leu Leu Ser Glu Asp Arg Thr Asp His Met Arg Gly
35 40 45

Ala Ser Thr Trp Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys
50 55 60

Asp Glu Cys Ile Leu Val Asp Val Glu Asp Asn Ile Thr Gly His Ala
65 70 75 80

Ser Lys Leu Glu Cys His Lys Phe Leu Pro His Gln Pro Ala Gly Leu
85 90 95

Leu His Arg Ala Phe Ser Val Phe Leu Phe Asp Asp Gln Gly Arg Leu
100 105 110

Leu Leu Gln Gln Arg Ala Arg Ser Lys Ile Thr Phe Pro Ser Val Trp
115 120 125

Thr Asn Thr Cys Cys Ser His Pro Leu His Gly Gln Thr Pro Asp Glu
130 135 140

Val Asp Gln Leu Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys
145 150 155 160

Ala Ala Ala Ile Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His
165 170 175

Gln Leu Pro Ala Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys

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            180                     185                     190

Ala Ala Asp Val Gln Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu
        195                     200                     205

His Glu Met Asp Tyr Ile Leu Phe Ile Arg Ala Asn Val Thr Leu Ala
    210                     215                     220

Pro Asn Pro Asp Glu Val Asp Glu Val Arg Tyr Val Thr Gln Glu Glu
225                     230                     235                     240

Leu Arg Gln Met Met Gln Pro Asp Asn Gly Leu Gln Trp Ser Pro Trp
                245                     250                     255

Phe Arg Ile Ile Ala Ala Arg Phe Leu Glu Arg Trp Trp Ala Asp Leu
            260                     265                     270

Asp Ala Ala Leu Asn Thr Asp Lys His Glu Asp Trp Gly Thr Val His
        275                     280                     285

His Ile Asn Glu Ala
    290

<210> 16
<211> 284
<212> PRT
<213> Arabidopsis thaliana

<400> 16
Met Ser Val Ser Ser Leu Phe Asn Leu Pro Leu Ile Arg Leu Arg Ser
  1               5                  10                  15

Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro
             20                  25                  30

Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser
         35                  40                  45

Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met Asp Ala Val Gln
     50                  55                  60

Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp
 65                  70                  75                  80

Arg Val Val Gly His Val Ser Lys Tyr Asn Cys His Leu Met Glu Asn
                 85                  90                  95

Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe
            100                 105                 110

Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val
        115                 120                 125

Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr
    130                 135                 140

Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala
145                 150                 155                 160

Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val
                165                 170                 175
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Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro
            180                 185                 190

Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile
        195                 200                 205

Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile
    210                 215                 220

Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp
225                 230                 235                 240

Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val
                245                 250                 255

Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu
            260                 265                 270

Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
        275                 280

<210> 17
<211> 287
<212> PRT
<213> Clarkia breweri

<400> 17
Met Ser Ser Ser Met Leu Asn Phe Thr Ala Ser Arg Ile Val Ser Leu
  1               5                  10                  15

Pro Leu Leu Ser Ser Pro Pro Ser Arg Val His Leu Pro Leu Cys Phe
             20                  25                  30

Phe Ser Pro Ile Ser Leu Thr Gln Arg Phe Ser Ala Lys Leu Thr Phe
         35                  40                  45

Ser Ser Gln Ala Thr Thr Met Gly Glu Val Val Asp Ala Gly Met Asp
     50                  55                  60

Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp
 65                  70                  75                  80

Glu Asn Asp Lys Val Val Gly His Glu Ser Lys Tyr Asn Cys His Leu
                 85                  90                  95

Met Glu Lys Ile Glu Ser Glu Asn Leu Leu His Arg Ala Phe Ser Val
            100                 105                 110

Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala
        115                 120                 125

Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His
    130                 135                 140

Pro Leu Tyr Arg Glu Ser Glu Leu Ile Asp Glu Asn Cys Leu Gly Val
145                 150                 155                 160

Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala
                165                 170                 175

Glu Asp Leu Pro Val Asp Gln Phe Ile Pro Leu Ser Arg Ile Leu Tyr
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180 185 190

Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu
195 200 205

Leu Phe Ile Ile Arg Asp Val Asn Leu Asp Pro Asn Pro Asp Glu Val
210 215 220

Ala Glu Val Lys Tyr Met Asn Arg Asp Asp Leu Lys Glu Leu Leu Arg
225 230 235 240

Lys Ala Asp Ala Glu Glu Glu Gly Val Lys Leu Ser Pro Trp Phe Arg
245 250 255

Leu Val Val Asp Asn Phe Leu Phe Lys Trp Trp Asp His Val Glu Lys
260 265 270

Gly Ser Leu Lys Asp Ala Ala Asp Met Lys Thr Ile His Lys Leu
275 280 285

<210> 18
<211> 261
<212> PRT
<213> Arabidopsis thaliana

<400> 18
Thr Gly Pro Pro Pro Arg Phe Phe Pro Ile Arg Ser Pro Val Pro Arg
1 5 10 15

Thr Gln Leu Phe Val Arg Ala Phe Ser Ala Val Thr Met Thr Asp Ser
20 25 30

Asn Asp Ala Gly Met Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp
35 40 45

Glu Cys Ile Leu Val Asp Glu Asn Asn Arg Val Val Gly His Asp Thr
50 55 60

Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala Glu Asn Leu Leu
65 70 75 80

His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu
85 90 95

Leu Gln Gln Arg Ser Lys Thr Lys Val Thr Phe Pro Leu Val Trp Thr
100 105 110

Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Glu
115 120 125

Glu Asn Val Leu Gly Val Arg Asn Ala Ala Gln Arg Lys Leu Phe Asp
130 135 140

Glu Leu Gly Ile Val Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro
145 150 155 160

Leu Gly Arg Met Leu Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu
165 170 175

His Glu Val Asp Tyr Leu Leu Phe Ile Val Arg Asp Val Lys Leu Gln
180 185 190

Pro Asn Pro Asp Glu Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu
195 200 205

Leu Lys Glu Leu Val Lys Lys Ala Asp Ala Gly Asp Glu Ala Val Lys
210 215 220

Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp
225 230 235 240

Trp Asp His Val Glu Lys Gly Thr Ile Thr Glu Ala Ala Asp Met Lys
245 250 255

Thr Ile His Lys Leu
260

<210> 19
<211> 288
<212> PRT
<213> Saccharomyces cerevisiae

<400> 19
Met Thr Ala Asp Asn Asn Ser Met Pro His Gly Ala Val Ser Ser Tyr
1 5 10 15

Ala Lys Leu Val Gln Asn Gln Thr Pro Glu Asp Ile Leu Glu Glu Phe
20 25 30

Pro Glu Ile Ile Pro Leu Gln Gln Arg Pro Asn Thr Arg Ser Ser Glu
35 40 45

Thr Ser Asn Asp Glu Ser Gly Glu Thr Cys Phe Ser Gly His Asp Glu
50 55 60

Glu Gln Ile Lys Leu Met Asn Glu Asn Cys Ile Val Leu Asp Trp Asp
65 70 75 80

Asp Asn Ala Ile Gly Ala Gly Thr Lys Lys Val Cys His Leu Met Glu
85 90 95

Asn Ile Glu Lys Gly Leu Leu His Arg Ala Phe Ser Val Phe Ile Phe
100 105 110

Asn Glu Gln Gly Glu Leu Leu Leu Gln Gln Arg Ala Thr Glu Lys Ile
115 120 125

Thr Phe Pro Asp Leu Trp Thr Asn Thr Cys Cys Ser His Pro Leu Cys
130 135 140

Ile Asp Asp Glu Leu Gly Leu Lys Gly Lys Leu Asp Asp Lys Ile Lys
145 150 155 160

Gly Ala Ile Thr Ala Ala Val Arg Lys Leu Asp His Glu Leu Gly Ile
165 170 175

Pro Glu Asp Glu Thr Lys Thr Arg Gly Lys Phe His Phe Leu Asn Arg
180 185 190

Ile His Tyr Met Ala Pro Ser Asn Glu Pro Trp Gly Glu His Glu Ile
195 200 205

Asp Tyr Ile Leu Phe Tyr Lys Ile Asn Ala Lys Glu Asn Leu Thr Val

210 215 220

Asn Pro Asn Val Asn Glu Val Arg Asp Phe Lys Trp Val Ser Pro Asn
225 230 235 240

Asp Leu Lys Thr Met Phe Ala Asp Pro Ser Tyr Lys Phe Thr Pro Trp
245 250 255

Phe Lys Ile Ile Cys Glu Asn Tyr Leu Phe Asn Trp Trp Glu Gln Leu
260 265 270

Asp Asp Leu Ser Glu Val Glu Asn Asp Arg Gln Ile His Arg Met Leu
275 280 285

<210> 20
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence of four plant B-cyclases

<400> 20
Met Asp Thr Leu Leu Lys Thr Pro Asn Leu Glu Phe Leu Pro His Gly
1 5 10 15

Phe Val Lys Ser Phe Ser Lys Phe Gly Lys Cys Glu Gly Val Cys Val
20 25 30

Lys Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr Lys Lys Glu Asn
35 40 45

Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys Gly Val Val Asp
50 55 60

Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu Ala Val Ala Gln Gln
65 70 75 80

Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile Asp Pro Pro Lys Leu
85 90 95

Ile Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu Phe Glu Ala Met
100 105 110

Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp Ser Gly Ala Val Tyr Ile
115 120 125

Asp Asp Thr Lys Asp Leu Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln
130 135 140

Leu Lys Ser Lys Met Met Gln Lys Cys Ile Asn Gly Val Lys Phe His
145 150 155 160

Gln Ala Lys Val Ile Lys Val Ile His Glu Glu Lys Ser Met Leu Ile
165 170 175

Cys Asn Asp Gly Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly
180 185 190

Phe Ser Arg Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln

195 200 205

Val Ala Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Lys
210 215 220

Met Val Phe Met Asp Trp Arg Asp Ser His Leu Asn Asn Glu Leu Lys
225 230 235 240

Glu Arg Asn Ser Ile Pro Thr Phe Leu Tyr Ala Met Pro Phe Ser Ser
245 250 255

Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg Pro Gly Leu
260 265 270

Arg Met Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu His Leu Gly
275 280 285

Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys Val Ile Pro Met
290 295 300

Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val Gly Ile Gly Gly
305 310 315 320

Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met Val Ala Arg Thr
325 330 335

Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile Tyr Leu Gly Ser
340 345 350

Glu Ser Ser Gly Glu Leu Ser Ala Glu Val Trp Lys Asp Leu Trp Pro
355 360 365

Ile Glu Arg Arg Arg Gln Arg Glu Phe Phe Cys Phe Gly Met Asp Ile
370 375 380

Leu Leu Lys Leu Asp Leu Pro Ala Thr Arg Arg Phe Phe Asp Ala Phe
385 390 395 400

Phe Asp Leu Glu Pro Arg Tyr Trp His Gly Phe Leu Ser Ser Arg Leu
405 410 415

Phe Leu Pro Glu Leu Ile Val Phe Gly Leu Ser Leu Phe Ser His Ala
420 425 430

Ser Asn Thr Ser Arg Glu Ile Met Thr Lys Gly Thr Pro Leu Val Met
435 440 445

Ile Asn Asn Leu Leu Gln Asp Glu
450 455

<210> 21
<211> 524
<212> PRT
<213> Arabidopsis thaliana

<400> 21
Met Glu Cys Val Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr
1 5 10 15

Phe Pro Ser Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr
20 25 30

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Ser Tyr Arg Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly
        35                  40                  45

Gly Gly Ser Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe
    50                  55                  60

Ala Asp Glu Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe
65                  70                  75                  80

Val Gln Met Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val
                85                  90                  95

Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val
            100                 105                 110

Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala
        115                 120                 125

Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
    130                 135                 140

Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
145                 150                 155                 160

Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp
                165                 170                 175

Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg
            180                 185                 190

Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
        195                 200                 205

Tyr Leu Ser Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu
    210                 215                 220

Arg Leu Val Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala
225                 230                 235                 240

Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val
                245                 250                 255

Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu
            260                 265                 270

Val Glu Asn Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr
        275                 280                 285

Arg Asp Tyr Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro
    290                 295                 300

Thr Phe Leu Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu
305                 310                 315                 320

Glu Thr Cys Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys
                325                 330                 335

Thr Lys Leu Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys
            340                 345                 350

Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro
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355 360 365

Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val
370 375 380

His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro
385 390 395 400

Lys Tyr Ala Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys
405 410 415

Gln Ile Asn Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro
420 425 430

Pro Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu
435 440 445

Ile Val Gln Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe
450 455 460

Phe Arg Leu Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu
465 470 475 480

Thr Ser Gly Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser
485 490 495

Pro Asn Asn Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro
500 505 510

Thr Gly Ala Thr Met Ile Lys Thr Tyr Leu Lys Val
515 520

<210> 22
<211> 1898
<212> DNA
<213> Adonis palaestina

<400> 22
AAAGGAGTGT TCTATTAATG TTACTGTCGC ATTCTTGCAA CACTTATATT CAAACTCCAT 60

TTTCTTCTTT TCTCTTCAAA ACAACAAACT AATGTGAGCA GAGTATCTGG CTATGGAACT 120

ACTTGGTGTT CGCAACCTCA TCTCTTCTTG CCCTGTGTGG ACTTTTGGAA CAAGAAACCT 180

TAGTAGTTCA AAACTAGCTT ATAACATACA TCGATATGGT TCTTCTTGTA GAGTAGATTT 240

TCAAGTGAGA GCTGATGGTG GAAGCGGGAG TAGAAGTTCT GTTGCTTATA AAGAGGGTTT 300

TGTGGATGAA GAGGATTTTA TCAAAGCTGG TGGTTCTGAG CTTTTGTTTG TCCAAATGCA 360

GCAAACAAAG TCTATGGAGA AACAGGCCAA GCTCGCCGAT AAGTTGCCAC CAATACCTTT 420

TGGAGAATCC GTGATGGACT TGGTTGTAAT AGGTTGTGGA CCTGCTGGTC TTTCACTGGC 480

TGCAGAAGCT GCTAAGCTAG GGTTGAAAGT TGGCCTTATT GGTCCTGATC TTCCTTTTAC 540

AAATAATTAT GGTGTGTGGG AAGACGAGTT CAAAGATCTT GGACTTGAAC GTTGTATCGA 600

GCATGCTTGG AAGGACACCA TCGTATATCT TGATAATGAT GCTCCTGTCC TTATTGGTCG 660

TGCATATGGA CGAGTTAGTC GACATTTGCT ACATGAGGAG TTGCTGAAAA GGTGTGTGGA 720

GTCAGGTGTA TCATATCTTG ATTCTAAAGT GGAAAGGATC ACTGAAGCTG GTGATGGCCA 780

TAGCCTTGTA GTTTGTGAAA ATGAGATCTT TATCCCTTGC AGGCTTGCTA CTGTTGCATC 840

TGGAGCAGCT TCAGGGAAAC TTTTGGAGTA TGAAGTAGGT GGCCCTCGTG TTTGTGTCCA 900

AACCGCTTAT GGGGTGGAGG TTGAGGTGGA GAACAATCCA TACGATCCCA ACTTAATGGT 960

ATTCATGGAC TACAGAGACT ATATGCAACA GAAATTACAG TGCTCGGAAG AAGAATATCC 1020

AACATTTCTC TATGTCATGC CCATGTCGCC AACAAGACTT TTTTTTGAGG AAACCTGTTT 1080

GGCCTCAAAA GATGCCATGC CATTCGATCT ACTGAAGAGA AAACTGATGT CACGATTGAA 1140

GACTCTGGGT ATCCAAGTTA CAAAAGTTTA TGAAGAGGAA TGGTCATATA TTCCTGTTGG 1200

TGGTTCTTTA CCAAACACAG AGCAAAAGAA CCTAGCATTT GGTGCTGCAG CAAGCATGGT 1260

GCATCCAGCA ACAGGCTATT CGGTTGTACG GTCACTGTCA GAAGCTCCAA AATATGCTTC 1320

TGTAATTGCA AAGATTTTGA AGCAAGATAA CTCTGCGTAT GTGGTTTCTG GACAAAGTAG 1380

TGCAGTAAAC ATTTCAATGC AAGCATGGAG CAGTCTTTGG CCAAAGGAGC GAAAACGTCA 1440

AAGAGCATTC TTTCTTTTTG GATTAGAGCT TATTGTGCAG CTAGATATTG AAGCAACCAG 1500

AACATTCTTT AGAACCTTCT TCCGCTTGCC AACTTGGATG TGGTGGGGTT TCCTTGGGTC 1560

TTCACTATCA TCTTTCGATC TCGTCTTGTT TTCCATGTAC ATGTTTGTTT TGGCGCCAAA 1620

CAGCATGAGG ATGTCACTTG TGAGACATTT GCTTTCAGAT CCTTCTGGTG CAGTTATGGT 1680

AAGAGCTTAC CTCGAAAGGT AGTCTCATCT ATTATTAAAC TCTAGTGTTT CACCAAATAA 1740

ATGAGGATCC TTCGAATGTG TATATGATCA TCTCTATGTA TATCCTGTAC TCTAATCTCA 1800

TAAAGTAAAT GCCGGGTTTG ATATTGTTGT GTCAAACCGG CCAATGATAT AAAGTAAATT 1860

TATTGATACA AAAGTAGTTT TTTTCCTTAA AAAAAAAA 1898

<210> 23
<211> 529
<212> PRT
<213> Adonis palaestina

<400> 23
Met Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp
1 5 10 15

Thr Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile
20 25 30

His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp
35 40 45

Gly Gly Ser Gly Ser Arg Ser Ser Val Ala Tyr Lys Glu Gly Phe Val
50 55 60

Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val
65 70 75 80

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Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp
                85                  90                  95

Lys Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val
            100                 105                 110

Ile Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys
        115                 120                 125

Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn
    130                 135                 140

Asn Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg
145                 150                 155                 160

Cys Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp
                165                 170                 175

Ala Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu
            180                 185                 190

Leu His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr
        195                 200                 205

Leu Asp Ser Lys Val Glu Arg Ile Thr Glu Ala Gly Asp Gly His Ser
    210                 215                 220

Leu Val Val Cys Glu Asn Glu Ile Phe Ile Pro Cys Arg Leu Ala Thr
225                 230                 235                 240

Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly
                245                 250                 255

Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val
            260                 265                 270

Glu Asn Asn Pro Tyr Asp Pro Asn Leu Met Val Phe Met Asp Tyr Arg
        275                 280                 285

Asp Tyr Met Gln Gln Lys Leu Gln Cys Ser Glu Glu Glu Tyr Pro Thr
    290                 295                 300

Phe Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu
305                 310                 315                 320

Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg
                325                 330                 335

Lys Leu Met Ser Arg Leu Lys Thr Leu Gly Ile Gln Val Thr Lys Val
            340                 345                 350

Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
        355                 360                 365

Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
    370                 375                 380

Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys
385                 390                 395                 400

Tyr Ala Ser Val Ile Ala Lys Ile Leu Lys Gln Asp Asn Ser Ala Tyr
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405 410 415

Val Val Ser Gly Gln Ser Ser Ala Val Asn Ile Ser Met Gln Ala Trp
420 425 430

Ser Ser Leu Trp Pro Lys Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
435 440 445

Phe Gly Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr
450 455 460

Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe
465 470 475 480

Leu Gly Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr
485 490 495

Met Phe Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His
500 505 510

Leu Leu Ser Asp Pro Ser Gly Ala Val Met Val Arg Ala Tyr Leu Glu
515 520 525

Arg

<210> 24
<211> 1370
<212> DNA
<213> Potato

<400> 24
TAGCGGAGGA TGAGTTCAAA GATCTTGGTC TTCAAGCCTG CATTGAACAT GTTTGGCTGG 60

GATACCATTG TATATCTTGA TGATGATGAT CCTATTCTTA TTGGCCGTGC CTATGGAAGA 120

GTTAGTCGCC ATTTACTGCA CGAGGAGTTA CTCAAAAGGT GTGTGGAGGC AGGTGTTTTG 180

TATCTAAACT CGAAAGTGGA TAGGATTGTT GAGGCCACAA ATGGCCACAG TCTTGTAGAG 240

TGCGAGGGTG ATGTTGTGAT TCCCTGCAGG TTTGTGACTG TTGCATCGGG AGCAGCCTCG 300

GGGAAATTCT TGCAGTATGA GTTGGGAGGT CCTAGAGTTT CTGTTCAAAC AGCTTATGGA 360

GTGGAAGTTG AGGTCGATAA CAATCCATTT GACCCGAGCC TGATGGTTTT CATGGATTAT 420

AGAGACTATG TCAGACACGA CGCTCAATCT TTAGAAGCTA AATATCCAAC ATTTCTCTAT 480

GCCATGCCCA TGTCTCCAAC ACGAGTCTTT TTCGAGGAAA CTTGTTTGGC TTCAAAAGAT 540

GCAATGCCAT TCGATCTGTT AAAGAAAAAA TTGATGTTAC GATTGAACAC CCTCGGTGTA 600

AGAATTAAAG AAATTTATGA GGAGGAATGG TCTTACATAC CAGTTGGAGG ATCTTTGCCA 660

AATACAGAAC AAAAAACACT TGCATTTGGT GCTGCTGCTA GCATGGTTCA TCCAGCCACA 720

GGTTATTCAG TCGTCAGATC ACTGTCTGAA GCTCCAAAAT GCGCCTTCGT GCTTGCAAAT 780

ATATTACGAC AAAATCATAG CAAGAATATG CTTACTAGTT CAAGTACCCC GAGTATTTCA 840

ACTCAAGCTT GGAACACTCT TTGGCCACAA GAACGAAAAC GACAAAGATC GTTTTTCCTA 900

TTTGGACTGG CTCTGATATT GCAGCTGGAT ATTGAGGGGA TAAGGTCATT TTTCCGCGCG 960

TTCTTCCGTG TGCCAAAATG GATGTGGCAG GGATTTCTTG GTTCAAGTCT TTCTTAGCAG 1020

ACCTCATGTT ATTTGCCTTC TACATGTTTA TTATTGCACC AAATGACATG AGAAGAGGCT 1080

TAATCAGACA TCTTTTATCT GATCCTACTG GTGCAACATT GATAAGAACT TATCTTACAT 1140

TTTAGAGTAA ATTCCTCCTA CAATAGTTGT TGAAAGAGGC CTCATTACTT CAGATTCATA 1200

ACAGAAATCG CGGTCTCTCG AGGCCTTGTA TATAACATTT TCACTAGGTT AATATTGCTT 1260

GAATAAGTTG CACAGTTTCA GTTTTTGTAT CTGCTTCTTT TTTGTCCAAG ATCATGTATT 1320

GACCAATTTA TATACATTGC CAGTATATAT AAATTTTATA AAAAAAAAAA 1370

<210> 25
<211> 377
<212> PRT
<213> Potato

<400> 25
Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile Glu His Val Trp
1 5 10 15

Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Asp Pro Ile Leu Ile Gly
20 25 30

Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu His Glu Glu Leu Leu
35 40 45

Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn Ser Lys Val Asp
50 55 60

Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val Glu Cys Glu Gly
65 70 75 80

Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala Ser Gly Ala Ala
85 90 95

Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Ser Val
100 105 110

Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn Asn Pro Phe Asp
115 120 125

Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Val Arg His Asp
130 135 140

Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu Tyr Ala Met Pro
145 150 155 160

Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys
165 170 175

Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met Leu Arg Leu
180 185 190

Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu Glu Glu Trp Ser
195 200 205

Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Thr Leu
210 215 220

Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser
225 230 235 240

Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala Phe Val Leu Ala
245 250 255

Asn Ile Leu Arg Gln Asn His Ser Lys Asn Met Leu Thr Ser Ser Ser
260 265 270

Thr Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu Trp Pro Gln Glu
275 280 285

Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu Ala Leu Ile Leu
290 295 300

Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg Ala Phe Phe Arg
305 310 315 320

Val Pro Lys Met Met Trp Gly Phe Leu Gly Ser Ser Leu Ser Xaa Ala
325 330 335

Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro Asn Asp
340 345 350

Met Arg Arg Gly Leu Ile Arg His Leu Leu Ser Asp Pro Thr Gly Ala
355 360 365

Thr Leu Ile Arg Thr Tyr Leu Thr Phe
370 375

<210> 26
<211> 533
<212> PRT
<213> Chimeric lettuce/potato

<400> 26
Met Glu Cys Phe Gly Ala Arg Asn Met Thr Ala Thr Met Ala Val Phe
1 5 10 15

Thr Cys Pro Arg Phe Thr Asp Cys Asn Ile Arg His Lys Phe Ser Leu
20 25 30

Leu Lys Gly Arg Arg Phe Thr Asn Leu Ser Ala Ser Ser Ser Leu Arg
35 40 45

Gln Ile Lys Cys Ser Ala Lys Ser Asp Arg Cys Val Val Asp Lys Gln
50 55 60

Gly Ile Ser Val Ala Asp Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser
65 70 75 80

Glu Leu Phe Phe Val Gln Met Gln Arg Thr Lys Ser Met Glu Ser Gln
85 90 95

Ser Lys Leu Ser Glu Lys Leu Ala Gln Ile Pro Ile Gly Asn Cys Ile
100 105 110

Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala

115 120 125

Ala Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu Ile Gly Pro Asp
130 135 140

Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Gln Asp Glu Phe Ile Gly
145 150 155 160

Leu Gly Leu Glu Gly Cys Ile Glu His Ser Trp Lys Asp Thr Leu Val
165 170 175

Tyr Leu Asp Asp Ala Asp Pro Ile Arg Ile Gly Arg Ala Tyr Gly Arg
180 185 190

Val His Arg Asp Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu
195 200 205

Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala
210 215 220

Pro Asn Gly Tyr Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro
225 230 235 240

Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Phe Leu
245 250 255

Glu Tyr Glu Leu Gly Gly Pro Arg Val Ser Val Gln Thr Ala Tyr Gly
260 265 270

Val Glu Val Glu Val Asp Asn Asn Pro Phe Asp Pro Ser Leu Met Val
275 280 285

Phe Met Asp Tyr Arg Asp Tyr Val Arg His Asp Ala Gln Ser Leu Glu
290 295 300

Ala Lys Tyr Pro Thr Phe Leu Tyr Ala Met Pro Met Ser Pro Thr Arg
305 310 315 320

Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe
325 330 335

Asp Leu Leu Lys Lys Lys Leu Met Leu Arg Leu Asn Thr Leu Gly Val
340 345 350

Arg Ile Lys Glu Ile Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly
355 360 365

Gly Ser Leu Pro Asn Thr Glu Gln Lys Thr Leu Ala Phe Gly Ala Ala
370 375 380

Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu
385 390 395 400

Ser Glu Ala Pro Lys Cys Ala Phe Val Leu Ala Asn Ile Leu Arg Gln
405 410 415

Asn His Ser Lys Asn Met Leu Thr Ser Ser Ser Thr Pro Ser Ile Ser
420 425 430

Thr Gln Ala Trp Asn Thr Leu Trp Pro Gln Glu Arg Lys Arg Gln Arg
435 440 445

Ser Phe Phe Leu Phe Gly Leu Ala Leu Ile Leu Gln Leu Asp Ile Glu
450 455 460

Gly Ile Arg Ser Phe Phe Arg Ala Phe Phe Arg Val Pro Lys Trp Met
465 470 475 480

Trp Gln Gly Phe Leu Gly Ser Ser Leu Ser Xaa Ala Asp Leu Met Leu
485 490 495

Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro Asn Asp Met Arg Arg Gly
500 505 510

Leu Ile Arg His Leu Leu Ser Asp Pro Thr Gly Ala Thr Leu Ile Arg
515 520 525

Thr Tyr Leu Thr Phe
530

<210> 27
<211> 374
<212> PRT
<213> Arabidopsis thaliana

<400> 27
Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln Lys Cys Ile Glu His Val
1 5 10 15

Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp Asp Lys Pro Ile Thr Ile
20 25 30

Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg Leu Leu His Glu Glu Leu
35 40 45

Leu Arg Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val
50 55 60

Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu Arg Leu Val Ala Cys Asp
65 70 75 80

Asp Asn Asn Val Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala
85 90 95

Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly Pro Arg Val Cys
100 105 110

Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Ser Pro Tyr
115 120 125

Asp Pro Asp Gln Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Asn Glu
130 135 140

Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro Thr Phe Leu Tyr Ala Met
145 150 155 160

Pro Met Thr Lys Ser Arg Leu Phe Phe Glu Glu Thr Cys Leu Ala Ser
165 170 175

Lys Asp Val Met Pro Phe Asp Leu Leu Lys Thr Lys Leu Met Leu Arg
180 185 190

Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys Thr Tyr Glu Glu Glu Trp

195 200 205

Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn
210 215 220

Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr
225 230 235 240

Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Tyr Ala Ser Val Ile
245 250 255

Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys Gln Ile Asn Ser Asn Ile
260 265 270

Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro Pro Glu Arg Lys Arg Gln
275 280 285

Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Phe Asp Thr
290 295 300

Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe Phe Arg Leu Pro Lys Trp
305 310 315 320

Met Trp Gln Gly Phe Leu Gly Ser Thr Leu Thr Ser Gly Asp Leu Val
325 330 335

Leu Phe Ala Leu Tyr Met Phe Val Ile Ser Pro Asn Asn Leu Arg Lys
340 345 350

Gly Leu Ile Asn His Leu Ile Ser Asp Pro Thr Gly Ala Thr Met Ile
355 360 365

Lys Thr Tyr Leu Lys Val
370

<210> 28
<211> 1002
<212> DNA
<213> Adonis palaestina

<400> 28
ATTCATCTTC AGCAGCGCTG TCGTACTCTT TCTATATCTT CTTCCATCAC TAACAGTAGT 60

CGCCGACGGT TGAATCGGCT ATTCGCCTCA ACGTCAACTA TGGGTGAAGT CACTGATGCT 120

GGAATGGATG CTGTTCAGAA GCGGCTCATG TTCGACGACG AATGTATTTT GGTGGATGAG 180

AATGACAAGG TCGTCGGGCA TGATTCCAAA TACAACTGTC ATTTGATGGA AAAGATAGAG 240

GCAGAAAATT TGCTTCACAG AGCCTTCAGT GTTTTCTTGT TCAACTCAAA ATATGAATTG 300

CTTCTTCAGC AACGATCCGC CACAAAGGTA ACATTCCCGC TCGTATGGAC AAACACATGT 360

TGCAGTCATC CTCTCTTTCG TGATTCCGAG CTCATAGAAG AAAATTATCT CGGTGTACGA 420

AACGCTGCAC AAAGAAAGCT TTTAGACGAG CTAGGCATTC CAGCTGAAGA TGTCCCAGTT 480

GATGAATTTA CTCCTCTTGG TCGCATTCTT TACAAAGCTC CATCTGACGG CAAATGGGGA 540

GAGCACGAAT TGGACTATCT CCTATTTATT GTCCGAGATG TGAAATACGA TCCAAACCCA 600

GATGAAGTTG CTGATGCTAA GTATGTTAAT CGCGAGGAGT TGAGAGAGAT ACTGAGAAAA 660

GCTGATGCTG GTGAAGAGGG ACTCAAGTTG TCTCCTTGGT TTAGATTGGT TGTTGATAAC 720

TTTTTGTTCA AGTGGTGGGA TCATGTAGAG CAGGGTACGA TTAAGGAAGT TGCTGACATG 780

AAAACTATCC ACAAGTTGAC TTAAGAGGAC TTCTCTCCTC TGTTCTACTA TTTGTTTTTT 840

GCTACAATAA GTGGGTGGTG ATAAGCAGTT TTTCTGTTTT CTTTAATTTA TGGCTTTTGA 900

ATTTGCCTCG ATGTTGAACT TGTAACATAT TTAGACAAAT ATGAGACCTT GTAAGTTGAA 960

TTTGAGGCTG AATTTATATT TTTGGGAACA TAATAATGTT AA 1002

<210> 29
<211> 1271
<212> DNA
<213> Adonis palaestina

<400> 29
TTTTAAAGCT CTTTCGCTCC ACCACCATCA AAGCCAGCCA AATTTCTCTG TACAAAAGTT 60

AAAAACACCG CTTTGGGCTT TGGCCCCTCC ATATCGGAAT CCTTGTTTAC GATACGCATC 120

TAAACCAGTA ATTCTCGGTT TTAATTTGTT TCCTAAATTA GGCCCCTTTC CGGAATCCCG 180

AGAATTATGT CGTCGATCAG GATTAATCCT TTATATAGTA TCTTCTCCAC CACCACTAAA 240

ACATTATCAG CTTCGTGTTC TTCTCCCGCT GTTCATCTTC AGCAGCGTTG TACGTACTCT 300

TTCTATTTCT TCTTCCATCA CTAACAGTCC TCGCCGAGGG TTGAATCGGC TGTTCGCCTC 360

AACGTCGACT ATGGGTGAAG TCGCTGATGC TGGTATGGAT GCCGTCCAGA AGCGGCTTAT 420

GTTCGACGAT GAATGTATTT TGGTGGATGA GAATGACAAG GTCGTCGGAC ATGATTCCAA 480

ATACAACTGT CATTTGATGG AAAAGATAGA GGCAGAAAAC TTGCTTCACA GAGCCTTCAG 540

TGTTTTCTTA TTCAACTCAA AATACGAGTT GCTTCTTCAG CAACGATCTG CAACGAAGGT 600

AACATTCCCG CTCGTATGGA CAAACACCTG TTGCAGCCAT CCCCTCTTCC GTGATTCCGA 660

ACTCATAGAA GAAAATTTTC TCGGGGTACG AAACGCTGCA CAAAGGAAGC TTTTAGACGA 720

GCTAGGCATT CCAGCTGAAG ACGTACCAGT TGATGAATTC ACTCCTCTTG GTCGCATTCT 780

TTACAAAGCT CCATCTGACG GAAAATGGGG AGAGCACGAA CTGGACTATC TTCTGTTTAT 840

TGTCCGAGAT GTGAAATACG ATCCAAACCC AGATGAAGTT GCTGACGCTA AGTACGTTAA 900

TCGCGAGGAG TTGAAAGAGA TACTGAGAAA AGCTGATGCA GGTGAAGAGG GAATAAAGTT 960

GTCTCCTTGG TTTAGATTGG TTGTGGATAA CTTTTTGTTC AAGTGGTGGG ATCATGTAGA 1020

GGAGGGGAAG ATTAAGGACG TCGCCGACAT GAAAACTATC CACAAGTTGA CTTAAGAGAA 1080

AGTCTCTTAA GTTCTACTAT TTGGTTTTTG CTTCAATAAG TGGATGGTGA TGAGCAGTTT 1140

TTATGCTTCC TTTAATTTTG GCTTTTCAAT TTGCTTTATG TGTTGAACTT GTAACATATT 1200

TAGTCAAATA TGAGACCTTG TGAGTTGAAT TTGAGGTTAT ATTTATAGTT TTGGGAACAT 1260

AAAAAAAAAA A 1271

<210> 30
<211> 1109
<212> DNA
<213> Haematococcus pluvialis

<400> 30
TGGAACCTGG CCCGGCGGCA GTCCGATGCC GCGATGCTTC GTTCGTTGCT CAGAGGCCTC 60

ACGCATATCC CGCGCGTGAA CTCCGCCCAG CAGCCCAGCT GTGCACACGC GCGACTCCAG 120

TTTAAGCTCA GGAGCATGCA GCTGCTTGCC GAGGACCGCA CAGACCACAT GAGGGGTGCA 180

AGCACCTGGG CAGGCGGGCA GTCGCAGGAT GAGCTGATGC TGAAGGACGA GTGCATCTTA 240

GTGGATGCTG ACGACAACAT CACAGGCCAT GCCAGCAAGC TGGAGTGCCA CAAATTCCTA 300

CCACATCAGC CTGCAGGCCT GCTGCACCGG GCCTTCTCTG TGTTCCTGTT TGACGACCAG 360

GGGCGACTGC TGCTGCAACA GCGTGCACGC TCAAAAATCA CCTTCCCAAG TGTGTGGACG 420

AACACCTGCT GCAGCCACCC TCTACATGGG CAGACCCCAG ATGAGGTGGA CCAACTAAGC 480

CAGGTGGCCG ACGGCACAGT ACCTGGCGCA AAAGCTGCTG CCATCCGCAA GTTGGAGCAC 540

GAGCTGGGGA TACCAGCGCA CCAGCTGCCG GCAAGCGCGT TTCGCTTCCT CACGCGTTTG 600

CACTACTGTG CCGCGGACGT GCAGCCGGCT GCGACACAAT CAGCGCTCTG GGGCGAGCAC 660

GAGATGGACT ACATCTTATT CATCCGGGCC AACGTCACCT TGGCGCCCAA CCCTGACGAG 720

GTGGACGAAG TCAGGTACGT GACGCAAGAG GAGCTGCGGC AGATGATGCA GCCGGACAAC 780

GGGTTGCAAT GGTCGCCGTG GTTTCGCATC ATCGCCGCGC GCTTCCTTGA GCGTTGGTGG 840

GCTGACCTGG ACGCGGCCCT AAACACTGAC AAACACGAGG ATTGGGGAAC GGTGCATCAC 900

ATCAACGAAG CGTGAAGGCA GAAGCTGCAG GATGTGAAGA CACGTCATGG GGTGGAATTG 960

CGTACTTGGC AGCTTCGTAT CTCCTTTTTC TGAGACTGAA CCTGCAGAGC TAGAGTCAAT 1020

GGTGCATCAT ATTCATCGTC TCTCTTTTGT TTTAGACTAA TCTGTAGCTA GAGTCACTGA 1080

TGAATCCTTT ACAACTTTCA AAAAAAAAA 1109

<210> 31
<211> 985
<212> DNA
<213> Lactuca sativa

<400> 31
TGCCAAAATG TTGAAATTTC CCCCTTTTAA AACCATTGCT ACCATGATCT CTTCTCCATA 60

TTCTTCCTTC TTGCTGCCTC GGAAATCTTC TTTCCCTCCA ATGCCGTCTC TCGCAGCCGC 120

TAGTGTTTTC CTCCACCCTC TTTCGTCTGC CGCTATGGGC GATTCCAGCA TGGATGCTGT 180

CCAGCGACGT CTCATGTTCG ATGACGAATG CATTTTGGTG GATGAGAATG ACAAAGTGGT 240

TGGCCATGAT ACTAAATACA ATTGTCATTT GATGGAGAAG ATTGAAAAGG GAAATATGCT 300

ACACAGAGCA TTCAGTGTGT TCTTGTTCAA CTCGAAATAT GAATTACTCC TTCAGCAACG 360

TTCTGCAACC AAGGTGACTT TCCCTTTGGT ATGGACAAAC ACGTGTTGCA GCCATCCACT 420

ATACAGGGAG AGTGAGCTTA TTGACGAAAA CGCCCTTGGG GTGAGGAATG CTGCACAGAG 480

GAAGCTCCTG GATGAACTCG GCATCCCTGG AGCAGATGTT CCGGTTGATG AGTTCACTCC 540

ATTGGGTCGC ATTCTATACA AGGCCGCATC GGATGGAAAG TGGGGAGAAC ATGAACTTGA 600

TTACCTGCTG TTTATGGTAC GTGATGTTGG TTTGGATCCG AACCCAGATG AAGTGAAAGA 660

TGTAAAATAT GTGAACCGGG AAGAGCTGAA GGAATTGGTA AGGAAGGCGG ATGCTGGTGA 720

AGAGGGTGTG AAGCTGTCCC CGTGGTTCAA ATTGATTGTC GATAATTTCT TGTTTCAGTG 780

GTGGGATCGA CTCCATAAGG GAACCCTAAC CGAAGCTATT GATATGAAAA CAATCCACAA 840

ACTCACATAA AAACACTACA CTAGTAGGAG AGAGGATTAT ATGAGATATT TGTTATATGT 900

GAAATTGAAA TTCAGATGAA TGCTTGTATT TATTTCTATT TGGACAAACT TCAACTTCTT 960

TTTGCTACCT TATCAGAAAA AAAAA 985

<210> 32
<211> 988
<212> DNA
<213> Lactuca sativa

<400> 32
TATTCGCTTC AAAATCTCTT CCATTAACTG CTCAAATCTC CACCTTCGCC GGTCTTAATC 60

TCCGCCGGCG CACTTTCACC ACCATAACCG CCGCCATGGG TGACGATTCC GGCATGGACG 120

CTGTCCAGAG ACGTCTCATG TTTGATGATG AATGCATTTT GGTTGATGAA AATGACAATG 180

TTCTTGGGCA TGATACCAAA TACAATTGTC ACTTGATGGA GAAGATTGAG AAAGATAATT 240

TGCTTCATAG AGCATTCAGT GTATTTTTAT TCAATTCAAA ATACGAATTA CTCCTTCAGC 300

AAAGGTCAGA AACCAAGGTG ACATTTCCTT TGGTATGGAC AAACACCTGT TGCAGCCATC 360

CACTATACAG AGAATCGGAG TTAATTCCCG AAAATGCCCT TGGGGTCAGA AATGCTGCAC 420

AGAGGAAGCT TCTAGATGAA CTCGGTATCC CTGCTGAAGA TGTTCCAGTT GATGAGTTCA 480

CAACTTTAGG TCGCATGTTG TACAAGGCTC CATCTGATGG AAAATGGGGT GAACATGAAG 540

TTGATTACCT ACTCTTCCTC GTGCGTGACG TTGCCGTGAA CCCAAACCCT GATGAGGTGG 600

CGGACATTAG ATACGTGAAC CAAGAAGAGT TAAAAGAGTT ACTAAGGAAG GCGGATGCGG 660

GTGAGGAGGG TTTGAAATTG TCCCCATGGT TTAGGCTAGT GGTGGACAAC TTCTTGTTCA 720

AATGGTGGGA TCATGTCCAA AAGGGGACAC TCAATGAAGC AATTGACATG AAAACCATTC 780

ATAAGTTGAT ATGAAAAATG GTTAATATTT ATGGTGGTGG TTTGGAGCTA ATAATTTGTG 840

TGTTCAAGTC TCGGTCCTTC TTTTTTTAAC GTTTTTTTTT TTTCTTTTAT TGGGAGTGTT 900

TATTGTGTAC TTGTAACGTA GGCCCTTTGG TTACGCTTTA AGAGTTTAAT AAAGAACCAC 960

CGTTAATTTA AAAAAAAAAA AAAAAAAA 988

<210> 33
<211> 1874
<212> DNA
<213> Chlamydomonas reinhardtii

<400> 33
GGCACGAGCT CGAGTTTGTT TTACCATGAC ATCGGGAATT TGGAAGCTTG AACTACCTCA 60

ATTACTCAAG TAACTCGCGG CAACACATTT CGCGCGCCAT CGCTGTTTTC TCTGCTCCAG 120

CTACCGAGCA GCATTGCTTT AGATCGCTTT GATGTCATAA ACTCCCACTT ATATGAGATC 180

CAGTTTCATC GAGCCCAAGC CCAGAGCGCA ACCTGTCTTA AGCCGCGGCA GGGCGTCCAT 240

GCGCCTCGCG CAAAGCCGTG CTCTCGTTGC GCGTGTCAGC TCCGCCCTGT GGCCGGGAGC 300

AGGACTTTCA CAGGCTCAAA GCGTTGCGGT GCGAATGGCG AGTTCGTCAA CCTGGGAAGG 360

CACGGGCCTG AGCCAGGATG ACTTCATGCA GCGGGACGAG TGCTTGGTGG TGGACGAGCA 420

GGACCGGCTG CTAGGCACCG CCAACAAGTA CGACTGCCAC CGCTTCGAGG CGGCCAAGGG 480

CCAGCCCTGC GGCCGCCTGC ACCGCGCCTT CTCCGTGTTC CTGTTCAGCC CCGACGGCCG 540

ACTGCTGCTG CAGCAGCGCG CAGCCAGCAA GGTGACGTTC CCGGGTGTGT GGACCAACAC 600

CTGCTGCTCG CACCCGCTGG CGGGCCAGGC GCCGGACGAG GTGGACCTGC CGGCGGCGGT 660

AGCCTCGGGC CAGGTGCCGG GCATCAAGGC GGCGGCGGTG CGCAAGCTGC AGCACGAGCT 720

GGGGATACCG CCGGAGCAGG TTCCCGCCTC CTCCTTCTCC TTCCTCACGC GTCTGCACTA 780

CTGCGCCGCC GACACCGCCA CGCACGGCCC GGCGGCGGAG TGGGGCGAGC ACGAGGTGGA 840

CTACGTGCTG TTCGTGCGGC CGCAGCAGCC CGTCAGCCTG CAGCCCAACC CAGACGAGGT 900

GGACGCCACG CGCTACGTGA CGCTGCCGGA GCTTCAGTCC ATGATGGCGG ACCCCGGCCT 960

CAGCTGGAGC CCCTGGTTCC GCATCCTGGC CACACAGCCC GCCTTCCTGC CCGCCTGGTG 1020

GGGCGACCTG AAGCGGCGCT GGCGCCCGGG CGGCAGCCGA CTGTCGGACT GGGGCACCAT 1080

CCACCGCGTC ATGTGAAGAA AAAGGGGAAG CAGGGGCGGG AGCGGGGGAT GAATGGGAAT 1140

GTGAATGCGA TTGTGATGCG GCGTGGGATG AGGTCTGAAG ACAGGGGGAA AATCGGGGGG 1200

CGGGCGTGAG CGTGTGTGTA CGTGAGCGAC AAAGCCGGGA GGCGGACCGC GCGATGGGTA 1260

CATGTGTGTG CGGAGGGTCG GTGGGTCGGT CGGTTGCGCG GCATAGCGTG TTGTGTGTGT 1320

GCGGCTGCAG GGGTATGTGG GCACCCGGGC ACGGAGGAGA AGGCACACGC AGGTGGCGCG 1380

GAGGTGTGTC AGGGGCCATG GGCGGGCCTC ACTCCTGGTC GTGCCCAGTG GTCTCGTGGG 1440

CAGAGTGGCA GGGGCTGCAC CCATATGAGC GGCGCACTGC CGCGCTGGGC TAAGTCCTTA 1500

TCACTTGGTG AGGTGGGGCG AGGTGGCTGT GGGCGGCGGG CGCAGTGGCA GAAGGACACG 1560

GTGTGTGAGC GGTGGAGCTC TGGCCGTGCC GGCCGTGAGG GGCGGATAGC GATATGACGT 1620

TGTGCTTGGC CGCTGTAATG CGGGAGAATG TGCAGGCCGC GAGAAGCGGG CGGTGGCAGG 1680

AGGCCGCAGG CTGCAGCACC CGTTGGGGAG GTGCCACCTG CAGGCGCGGC GCCGGGCGGG 1740

CCTGAGTAAT GGGCGCCTGA GTAGTGGCGG CCACAGGAGG CGCAGGAGGC AGCAGCAGGA 1800

GGACGAGCTG GAGGGACCCG TTGGCAACCC AAGGTTGCGC GTGTAACATA GTGGCCATAC 1860

AAAAAAAAAA AAAA 1874

<210> 34
<211> 954
<212> DNA
<213> Tagetes erecta

<400> 34
CCAAAAACAA CTCAAATCTC CTCCGTCGCT CTTACTCCGC CATGGGTGAC GACTCCGGCA 60

TGGATGCTGT TCAGCGACGT CTCATGTTTG ACGATGAATG CATTTTGGTG GATGAGTGTG 120

ACAATGTGGT GGGACATGAT ACCAAATACA ATTGTCACTT GATGGAGAAG ATTGAAACAG 180

GTAAAATGCT GCACAGAGCA TTCAGCGTTT TTCTATTCAA TTCAAAATAC GAGTTACTTC 240

TTCAGCAACG GTCTGCAACC AAGGTGACAT TTCCTTTAGT ATGGACCAAC ACCTGTTGCA 300

GCCATCCACT CTACAGAGAA TCCGAGCTTG TTCCCGAAAA CGCCCTTGGA GTAAGAAATG 360

CTGCACAGAG GAAGCTGTTG GATGAACTCG GTATCCCTGC TGAAGATGTT CCCGTTGATC 420

AGTTTACTCC TTTAGGTCGC ATGCTCTACA AGGCTCCATC TGATGGAAAG TGGGGAGAAC 480

ATGAACTTGA CTACCTACTT TTCATAGTGA GAGACGTTGC TGTAAACCCG AACCCAGATG 540

AAGTGGCGGA TATCAAATAT GTGACCAGAA GAGTTAAAGG AGCTGCTAAG GAAAGCAGAT 600

GCGGGGGAGG AGGGTTTGAA GCTGTCTCCA TGGTTCAGGT TAGTGGTTGA TAACTTCTTG 660

TTCAAGTGGT GGGATCATGT GCAAAAGGGT ACACTCACTG AAGCAATTGA TATGAAAACC 720

ATACACAAGC TGATATAGAA ACACACCCTC AACCGAAAAG TTCAAGCCTA ATAATTCGGG 780

TTGGGTCGGG TCTACCATCA ATTGTTTTTT TCTTTTAAGA AGTTTTAATC TCTATTTGAG 840

CATGTTGATT CTTGTCTTTT GTGTGTAAGA TTTTGGGTTT CGTTTCAGTT GTAATAATGA 900

ACCATTGATG GTTTGCAATT TCAAGTTCCT ATCGACATGT AGTGATCTAA AAAA 954

<210> 35
<211> 1031
<212> DNA
<213> Oryza sativa

<400> 35
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GCCGCCGCCG TGGAGGACGC CGGGATGGAC GAGGTCCAGA AGCGGCTCAT GTTCGACGAC 120

GAATGCATTT TGGTGGATGA ACAAGACAAT GTTGTTGGCC ATGAATCAAA ATATAACTGC 180

CATCTGATGG AAAAAATCGA ATCTGAAAAT CTACTTCATA GGGCTTTCAG TGTATTCCTG 240

TTCAACTCAA AATATGAACT CCTACTCCAG CAACGATCTG CAACAAAGGT TACATTTCCT 300

CTAGTTTGGA CCAACACTTG CTGCAGCCAT CCTCTGTACC GTGAGTCTGA GCTTATACAG 360

GAAAACTACC TTGGTGTTAG AAATGCTGCT CAGAGGAAGC TCTTGGATGA GCTGGGCATC 420

CCAGCTGAAG ATGTGCCAGT TGACCAATTC ACCCCTCTTG GTCGGATGCT TTACAAGGCC 480

CCATCTGATG GAAAATGGGG TGAACACGAG CTTGACTACC TGCTGTTCAT CGTCCGCGAC 540

GTGAAGGTAG TCCCGAACCC GGACGAAGTG GCCGATGTGA AATACGTGAG CCGTGAGCAG 600

CTGAAGGAGC TCATCCGCAA AGCGGACGCC GGAGAGGAAG GCCTGAAGCT GTCTCCCTGG 660

TTCCGGCTGG TTGTTGACAA CTTCCTCATG GGCTGGTGGG ATCACGTCGA GAAAGGCACC 720

CTCAACGAGG CCGTGGACAT GGAGACCATC CACAAGCTGA AGTAAGGACT GCGATGTTGT 780

GGCTGGAAAG AATGATCCTG AAGACTCTGT TCTTGTGCTG CTGCATATTA CTCTTACCAG 840

GGAAGTTGCA GAAGTCAGAA GAAGCTTTTG TATGTTTCTG GGTTTGGAGC TTGGAAGTGT 900

TGGGCTCTGC TGACTGAGAG ATTCCCTTAT AGAGTGTCTA TGTTAATTTA GCAAACTTCT 960

ATATTATACA TGATTAGTTA ATTGTTCGGT GTCTGAATAA AGAACAATAG CATGTTCCAT 1020

GTTTATTTGC T 1031

<210> 36
<211> 232
<212> PRT
<213> Tagetes erecta

<400> 36
Met Gly Asp Asp Ser Gly Met Asp Ala Val Gln Arg Arg Leu Met Phe
1 5 10 15

Asp Asp Glu Cys Ile Leu Val Asp Glu Cys Asp Asn Val Val Gly His
20 25 30

Asp Thr Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Thr Gly Lys
35 40 45

Met Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu
50 55 60

Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro Leu Val
65 70 75 80

Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser Glu Leu
85 90 95

Val Pro Glu Asn Ala Leu Gly Val Arg Asn Ala Ala Gln Arg Lys Leu
100 105 110

Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp Gln Phe
115 120 125

Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro Ser Asp Gly Lys Trp
130 135 140

Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp Val Ala
145 150 155 160

Val Asn Pro Asn Pro Asp Glu Val Ala Asp Ile Lys Tyr Val Ser His
165 170 175

Glu Glu Leu Lys Glu Leu Leu Arg Lys Ala Asp Ala Gly Glu Glu Gly
180 185 190

Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe Leu Phe
195 200 205

Lys Trp Trp Asp His Val Gln Lys Gly Thr Leu Thr Glu Ala Ile Asp
210 215 220

Met Lys Thr Ile His Lys Leu Ile
225 230

<210> 37
<211> 280
<212> PRT
<213> Lactuca Sativa

<400> 37
Met Leu Lys Phe Pro Pro Phe Lys Thr Ile Ala Thr Met Ile Ser Ser
1 5 10 15

Pro Tyr Ser Ser Phe Leu Leu Pro Arg Lys Ser Ser Phe Pro Pro Met
20 25 30

Pro Ser Leu Ala Ala Ala Ser Val Phe Leu His Pro Leu Ser Ser Ala
35 40 45

Ala Met Gly Asp Ser Ser Met Asp Ala Val Gln Arg Arg Leu Met Phe
50 55 60

Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val Gly His
65 70 75 80

Asp Thr Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Lys Gly Asn
85 90 95

Met Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu
100 105 110

Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro Leu Val
115 120 125

Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser Glu Leu
130 135 140

Ile Asp Glu Asn Ala Leu Gly Val Arg Asn Ala Ala Gln Arg Lys Leu
145 150 155 160

Leu Asp Glu Leu Gly Ile Pro Gly Ala Asp Val Pro Val Asp Glu Phe
165 170 175

Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Ala Ser Asp Gly Lys Trp
180 185 190

Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Met Val Arg Asp Val Gly

195 200 205

Leu Asp Pro Asn Pro Asp Glu Val Lys Asp Val Lys Tyr Val Asn Arg
210 215 220

Glu Glu Leu Lys Glu Leu Val Arg Lys Ala Asp Ala Gly Glu Glu Gly
225 230 235 240

Val Lys Leu Ser Pro Trp Phe Lys Leu Ile Val Asp Asn Phe Leu Phe
245 250 255

Gln Trp Trp Asp Arg Leu His Lys Gly Thr Leu Thr Glu Ala Ile Asp
260 265 270

Met Lys Thr Ile His Lys Leu Thr
275 280

<210> 38
<211> 229
<212> PRT
<213> Lactuca Sativa

<400> 38
Met Gly Asp Asp Ser Gly Met Asp Ala Val Gln Arg Arg Leu Met Phe
1 5 10 15

Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Asn Val Leu Gly His
20 25 30

Asp Thr Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Lys Asp Asn
35 40 45

Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu
50 55 60

Leu Leu Leu Gln Gln Arg Ser Glu Thr Lys Val Thr Phe Pro Leu Val
65 70 75 80

Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser Glu Leu
85 90 95

Ile Pro Glu Asn Ala Leu Gly Val Arg Asn Ala Ala Gln Arg Lys Leu
100 105 110

Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp Glu Phe
115 120 125

Thr Thr Leu Gly Arg Met Leu Tyr Lys Ala Pro Ser Asp Gly Lys Trp
130 135 140

Gly Glu His Glu Val Asp Tyr Leu Leu Phe Leu Val Arg Asp Val Ala
145 150 155 160

Val Asn Pro Asn Pro Asp Glu Val Ala Asp Ile Arg Tyr Val Asn Gln
165 170 175

Glu Glu Leu Lys Glu Leu Leu Arg Lys Ala Asp Ala Gly Glu Glu Gly
180 185 190

Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe Leu Phe
195 200 205

Lys Trp Trp Asp His Val Gln Lys Gly Thr Leu Asn Glu Ala Ile Asp
210 215 220

Met Lys Thr Ile His
225

<210> 39
<211> 295
<212> PRT
<213> Adonis Palaestina

<400> 39
Met Ser Ser Ile Arg Ile Asn Pro Leu Tyr Ser Ile Phe Ser Thr Thr
1 5 10 15

Thr Lys Thr Leu Ser Ala Ser Cys Ser Ser Pro Ala Val His Leu Gln
20 25 30

Gln Arg Cys Arg Thr Leu Ser Ile Ser Ser Ser Ile Thr Asn Ser Pro
35 40 45

Arg Arg Gly Leu Asn Arg Leu Phe Ala Ser Thr Ser Thr Met Gly Glu
50 55 60

Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu Met Phe Asp
65 70 75 80

Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val Gly Tyr Asp
85 90 95

Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala Glu Asn Leu
100 105 110

Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu
115 120 125

Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro Leu Val Trp
130 135 140

Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser Glu Leu Ile
145 150 155 160

Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg Lys Leu Leu
165 170 175

Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp Glu Phe Thr
180 185 190

Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly
195 200 205

Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp Val Lys Tyr
210 215 220

Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val Asn Arg Glu
225 230 235 240

Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu Glu Gly Ile
245 250 255

Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe Leu Phe Lys

260 265 270

Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val Ala Asp Met
275 280 285

Lys Thr Ile His Lys Leu Thr
290 295

<210> 40
<211> 234
<212> PRT
<213> Adonis Palaestina

<400> 40
Met Gly Glu Val Thr Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu
1 5 10 15

Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val
20 25 30

Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
35 40 45

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
50 55 60

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
65 70 75 80

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser
85 90 95

Glu Leu Ile Glu Glu Asn Tyr Leu Gly Val Arg Asn Ala Ala Gln Arg
100 105 110

Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
115 120 125

Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
130 135 140

Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
145 150 155 160

Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
165 170 175

Asn Arg Glu Glu Leu Arg Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
180 185 190

Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
195 200 205

Leu Phe Lys Trp Trp Asp His Val Glu Gln Gly Thr Ile Lys Glu Val
210 215 220

Ala Asp Met Lys Thr Ile His Lys Leu Thr
225 230

<210> 41
<211> 238

<212> PRT
<213> Oryza Sativa

<400> 41
Met Ala Gly Ala Ala Ala Ala Val Glu Asp Ala Gly Met Asp Glu Val
1 5 10 15

Gln Lys Arg Leu Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Gln
20 25 30

Asp Asn Val Val Gly His Glu Ser Lys Tyr Asn Cys His Leu Met Glu
35 40 45

Lys Ile Glu Ser Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu
50 55 60

Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys
65 70 75 80

Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu
85 90 95

Tyr Arg Glu Ser Glu Leu Ile Gln Glu Asn Tyr Leu Gly Val Arg Asn
100 105 110

Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp
115 120 125

Val Pro Val Asp Gln Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala
130 135 140

Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe
145 150 155 160

Ile Val Arg Asp Val Lys Val Val Pro Asn Pro Asp Glu Val Ala Asp
165 170 175

Val Lys Tyr Val Ser Arg Glu Gln Leu Lys Glu Leu Ile Arg Lys Ala
180 185 190

Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val
195 200 205

Val Asp Asn Phe Leu Met Gly Trp Trp Asp His Val Glu Lys Gly Thr
210 215 220

Leu Asn Glu Ala Val Asp Met Glu Thr Ile His Lys Leu Lys
225 230 235

<210> 42
<211> 233
<212> PRT
<213> Arabidopsis thaliana

<400> 42
Met Thr Asp Ser Asn Asp Ala Gly Met Asp Ala Val Gln Arg Arg Leu
1 5 10 15

Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Asn Asn Arg Val Val
20 25 30

Gly His Asp Thr Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
35 40 45

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
50 55 60

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Lys Thr Lys Val Thr Phe Pro
65 70 75 80

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr Arg Glu Ser
85 90 95

Glu Leu Ile Glu Glu Asn Val Leu Gly Val Arg Asn Ala Ala Gln Arg
100 105 110

Lys Leu Phe Asp Glu Leu Gly Ile Val Ala Glu Asp Val Pro Val Asp
115 120 125

Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro Ser Asp Gly
130 135 140

Lys Trp Gly Glu His Glu Val Asp Tyr Leu Leu Phe Ile Val Arg Asp
145 150 155 160

Val Lys Leu Gln Pro Asn Pro Asp Glu Val Ala Glu Ile Lys Tyr Val
165 170 175

Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp Ala Gly Asp
180 185 190

Glu Ala Val Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
195 200 205

Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Ile Thr Glu Ala
210 215 220

Ala Asp Met Lys Thr Ile His Lys Leu
225 230

<210> 43
<211> 293
<212> PRT
<213> Haematococcus pluvialis

<400> 43
Met Leu Arg Ser Leu Leu Arg Gly Leu Thr His Ile Pro Arg Val Asn
1 5 10 15

Ser Ala Gln Gln Pro Ser Cys Ala His Ala Arg Leu Gln Phe Lys Leu
20 25 30

Arg Ser Met Gln Leu Leu Ser Glu Asp Arg Thr Asp His Met Arg Gly
35 40 45

Ala Ser Thr Trp Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys
50 55 60

Asp Glu Cys Ile Leu Val Asp Val Glu Asp Asn Ile Thr Gly His Ala
65 70 75 80

Ser Lys Leu Glu Cys His Lys Phe Leu Pro His Gln Pro Ala Gly Leu

85 90 95

Leu His Arg Ala Phe Ser Val Phe Leu Phe Asp Asp Gln Gly Arg Leu
100 105 110

Leu Leu Gln Gln Arg Ala Arg Ser Lys Ile Thr Phe Pro Ser Val Trp
115 120 125

Thr Asn Thr Cys Cys Ser His Pro Leu His Gly Gln Thr Pro Asp Glu
130 135 140

Val Asp Gln Leu Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys
145 150 155 160

Ala Ala Ala Ile Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His
165 170 175

Gln Leu Pro Ala Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys
180 185 190

Ala Ala Asp Val Gln Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu
195 200 205

His Glu Met Asp Tyr Ile Leu Phe Ile Arg Ala Asn Val Thr Leu Ala
210 215 220

Pro Asn Pro Asp Glu Val Asp Glu Val Arg Tyr Val Thr Gln Glu Glu
225 230 235 240

Leu Arg Gln Met Met Gln Pro Asp Asn Gly Leu Gln Trp Ser Pro Trp
245 250 255

Phe Arg Ile Ile Ala Ala Arg Phe Leu Glu Arg Trp Trp Ala Asp Leu
260 265 270

Asp Ala Ala Leu Asn Thr Asp Lys His Glu Asp Trp Gly Thr Val His
275 280 285

His Ile Asn Glu Ala
290

<210> 44
<211> 304
<212> PRT
<213> Haematococcus pluvialis

<400> 44
Met Leu Arg Ser Leu Leu Arg Gly Leu Thr His Ile Pro Arg Val Asn
1 5 10 15

Ser Ala Gln Gln Pro Ser Cys Ala His Ala Arg Leu Gln Phe Lys Leu
20 25 30

Arg Ser Met Gln Met Thr Leu Met Gln Pro Ser Ile Ser Ala Asn Leu
35 40 45

Ser Arg Ala Glu Asp Arg Thr Asp His Met Arg Gly Ala Ser Thr Trp
50 55 60

Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys Asp Glu Cys Ile
65 70 75 80

Leu Val Asp Val Glu Asp Asn Ile Thr Gly His Ala Ser Lys Leu Glu
85 90 95

Cys His Lys Phe Leu Pro His Pro Ala Gly Leu Leu His Arg Ala Phe
100 105 110

Ser Val Phe Leu Phe Asp Asp Gln Gly Arg Leu Leu Leu Gln Gln Arg
115 120 125

Ala Arg Ser Lys Ile Thr Phe Pro Ser Val Trp Thr Asn Thr Cys Cys
130 135 140

Ser His Pro Leu His Gly Gln Thr Pro Asp Glu Val Asp Gln Leu Ser
145 150 155 160

Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys Ala Ala Ala Ile Arg
165 170 175

Lys Leu Glu His Glu Leu Gly Ile Pro Ala His Gln Leu Pro Ala Ser
180 185 190

Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys Ala Ala Asp Val Gln
195 200 205

Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu His Glu Met Asp Tyr
210 215 220

Ile Leu Phe Ile Arg Ala Asn Val Thr Leu Ala Pro Asn Pro Asp Glu
225 230 235 240

Val Asp Glu Val Arg Tyr Val Thr Gln Glu Glu Leu Arg Gln Met Met
245 250 255

Gln Pro Asp Asn Gly Leu Gln Trp Ser Pro Trp Phe Arg Ile Ile Ala
260 265 270

Ala Arg Phe Leu Glu Arg Trp Trp Ala Asp Leu Asp Ala Ala Leu Asn
275 280 285

Thr Asp Lys His Glu Asp Trp Gly Thr Val His His Ile Asn Glu Ala
290 295 300

<210> 45
<211> 307
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 45
Met Arg Ser Ser Phe Ile Glu Pro Lys Pro Arg Ala Gln Pro Val Leu
1 5 10 15

Ser Arg Gly Arg Ala Ser Met Arg Leu Ala Gln Ser Arg Ala Leu Val
20 25 30

Ala Arg Val Ser Ser Ala Leu Trp Pro Gly Ala Gly Leu Ser Gln Ala
35 40 45

Gln Ser Val Ala Val Arg Met Ala Ser Ser Ser Thr Trp Glu Gly Thr
50 55 60

Gly Leu Ser Gln Asp Asp Phe Met Gln Arg Asp Glu Cys Leu Val Val

65 70 75 80

Asp Glu Gln Asp Arg Leu Leu Gly Thr Ala Asn Lys Tyr Asp Cys His
85 90 95

Arg Phe Glu Ala Ala Lys Gly Gln Pro Cys Gly Arg Leu His Arg Ala
100 105 110

Phe Ser Val Phe Leu Phe Ser Pro Asp Gly Arg Leu Leu Leu Gln Gln
115 120 125

Arg Ala Ala Ser Lys Val Thr Phe Pro Gly Val Trp Thr Asn Thr Cys
130 135 140

Cys Ser His Pro Leu Ala Gly Gln Ala Pro Asp Glu Val Asp Leu Pro
145 150 155 160

Ala Ala Val Ala Ser Gly Gln Val Pro Gly Ile Lys Ala Ala Ala Val
165 170 175

Arg Lys Leu Gln His Glu Leu Gly Ile Pro Pro Glu Gln Val Pro Ala
180 185 190

Ser Ser Phe Ser Phe Leu Thr Arg Leu His Tyr Cys Ala Ala Asp Thr
195 200 205

Ala Thr His Gly Pro Ala Ala Glu Trp Gly Glu His Glu Val Asp Tyr
210 215 220

Val Leu Phe Val Arg Pro Gln Gln Pro Val Ser Leu Gln Pro Asn Pro
225 230 235 240

Asp Glu Val Asp Ala Thr Arg Tyr Val Thr Leu Pro Glu Leu Gln Ser
245 250 255

Met Met Ala Asp Pro Gly Leu Ser Trp Ser Pro Trp Phe Arg Ile Leu
260 265 270

Ala Thr Gln Pro Ala Phe Leu Pro Ala Trp Trp Gly Asp Leu Lys Arg
275 280 285

Arg Trp Arg Pro Gly Gly Ser Arg Leu Ser Asp Trp Gly Thr Ile His
290 295 300

Arg Val Met
305

<210> 46
<211> 1848
<212> DNA
<213> Adonis palaestina

<400> 46
GAGAGAAAAA GAGTGTTATA TTAATGTTAC TGTCGCATTC TTGCAACACA TATTCAGACT 60

CCATTTTCTT GTTTTCTCTT CAAAACAACA AACTAATGTG ACGGAGTATC TAGCTATGGA 120

ACTACTTGGT GTTCGCAACC TCATCTCTTC TTGCCCTGTC TGGACTTTTG GAACAAGAAA 180

CCTTAGTAGT TCAAAACTAG CTTATAACAT ACATCGATAT GGTTCTTCTT GTAGAGTAGA 240

TTTTCAAGTG AGGGCTGATG GTGGAAGCGG GAGTAGAACT TCTGTTGCTT ATAAAGAGGG 300

TTTTGTGGAC GAGGAGGATT TTATCAAAGC TGGTGGTTCT GAGCTTTTGT TTGTCCAAAT 360

GCAGCAAACA AAGTCTATGG AGAAACAGGC CAAGCTCGCC GATAAGTTGC CACCAATACC 420

TTTCGGAGAA TCTGTGATGG ACTTGGTTGT AATAGGTTGT GGACCTGCTG GTCTTTCACT 480

GGCTGCAGAA GCTGCTAAGC TAGGCTTGAA AGTTGGCCTT ATTGGTCCTG ATCTTCCTTT 540

TACAAATAAT TATGGTGTGT GGGAAGACGA GTTCAAAGAT CTTGGACTTG AACGTTGTAT 600

CGAGCATGCT TGGAAGGACA CCATCGTATA TCTTGACAAT GATGCTCCTG TCCTTATTGG 660

TCGTGCATAT GGACGAGTTA GCCGGCATTT GCTGCATGAA GAGTTGCTGA AAAGGTGTGT 720

CGAGTCAGGT GTATCATATC TGAATTCTAA AGTGGAAAGG ATCACTGAAG CTGGTGATGG 780

CCATAGTCTT GTAGTTTGTG AAAACGACAT CTTTATCCCT TGCAGGCTTG CTACTGTTGC 840

ATCTGGAGCA GCTTCAGGGA AACTTTTGGA GTATGAAGTA GGTGGCCCTC GTGTTTGTGT 900

CCAAACTGCT TATGGTGTGG AGGTTGAGGT GGAGAACAAT CCATACGATC CCAACTTAAT 960

GGTATTTATG GACTACAGAG ACTATATGCA ACAGAAATTA CAGTGCTCGG AAGAAGAATA 1020

TCCAACATTT CTCTATGTCA TGCCCATGTC GCCAACAAGA CTTTTTTTTG AGGAAACCTG 1080

TTTGGCCTCA AAAGATGCCA TGCCTTTCGA TCTACTGAAG AGAAAACTAA TGTCACGATT 1140

GAAGACTCTG GGTATCCAAG TTACAAAAAT TTATGAAGAG GAATGGTCTT ATATTCCTGT 1200

TGGGGGTTCT TTACCAAACA CAGAGCAAAA GAACCTAGCA TTTGGTGCTG CAGCAAGCAT 1260

GGTGCATCCA GCAACAGGCT ATTCGGTTGT ACGATCACTA TCAGAAGCTC CAAAATATGC 1320

TTCTGTAATT GCAAAGATTT TGAAGCAAGA TAACTCTGCA TATGTGGTTT CTGGACAAAG 1380

CAGTGCAGTA AACATTTCAA TGCAAGCATG GAGCAGTCTT TGGCCAAAGG AGCGAAAACG 1440

TCAAAGAGCA TTCTTTCTTT TCGGGTTAGA GCTTATTGTG CAGCTAGATA TTGAAGCAAC 1500

CAGAACGTTC TTTAGAACCT TCTTCCGCTT GCCAACTTGG ATGTGGTGGG GTTTCCTTGG 1560

GTCTTCACTA TCATCTTTCG ATCTTGTATT GTTTTCCATG TACATGTTTG TTTTGGCCCC 1620

GAACAGCATG AGGATGTCAC TTGTGAGACA TTTGCTTTCA GATCCTTCTG GTGCAGTTAT 1680

GGTTAAAGCT TACCTCGAAA GGTAATCTGT TTTATGAAAC TATAGTGTCT CATTAAATAA 1740

ATGAGGATCC TTCGTATATG TATATGATCA TCTCTATGTA TATCCTATAT TCTAATCTCA 1800

TAAAGTAATC GAAAATTCAT TGATAGAAAA AAAAAAAAAA AAAAAAAA 1848

<210> 47
<211> 529
<212> PRT
<213> Adonis palaestina

<400> 47
Met Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp

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1               5                   10                  15
Thr Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile
            20                  25                  30
His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp
        35                  40                  45
Gly Gly Ser Gly Ser Arg Ser Ser Val Ala Tyr Lys Glu Gly Phe Val
    50                  55                  60
Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val
65                  70                  75                  80
Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp
                85                  90                  95
Lys Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val
            100                 105                 110
Ile Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys
        115                 120                 125
Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn
    130                 135                 140
Asn Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg
145                 150                 155                 160
Cys Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp
                165                 170                 175
Ala Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu
            180                 185                 190
Leu His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr
        195                 200                 205
Leu Asp Ser Lys Val Glu Arg Ile Thr Glu Ala Gly Asp Gly His Ser
    210                 215                 220
Leu Val Val Cys Glu Asn Glu Ile Phe Ile Pro Cys Arg Leu Ala Thr
225                 230                 235                 240
Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly
                245                 250                 255
Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val
            260                 265                 270
Glu Asn Asn Pro Tyr Asp Pro Asn Leu Met Val Phe Met Asp Tyr Arg
        275                 280                 285
Asp Tyr Met Gln Gln Lys Leu Gln Cys Ser Glu Glu Glu Tyr Pro Thr
    290                 295                 300
Phe Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu
305                 310                 315                 320
Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg
                325                 330                 335
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Lys Leu Met Ser Arg Leu Lys Thr Leu Gly Ile Gln Val Thr Lys Val
340 345 350

Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
355 360 365

Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
370 375 380

Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys
385 390 395 400

Tyr Ala Ser Val Ile Ala Lys Ile Leu Lys Gln Asp Asn Ser Ala Tyr
405 410 415

Val Val Ser Gly Gln Ser Ser Ala Val Asn Ile Ser Met Gln Ala Trp
420 425 430

Ser Ser Leu Trp Pro Lys Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
435 440 445

Phe Gly Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr
450 455 460

Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe
465 470 475 480

Leu Gly Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr
485 490 495

Met Phe Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His
500 505 510

Leu Leu Ser Asp Pro Ser Gly Ala Val Met Val Arg Ala Tyr Leu Glu
515 520 525

Arg

<210> 48
<211> 378
<212> PRT
<213> Potato

<400> 48
Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile Glu His Val Trp
1 5 10 15

Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Asp Pro Ile Leu Ile Gly
20 25 30

Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu His Glu Glu Leu Leu
35 40 45

Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn Ser Lys Val Asp
50 55 60

Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val Glu Cys Glu Gly
65 70 75 80

Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala Ser Gly Ala Ala
85 90 95

Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Ser Val
100 105 110

Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn Asn Pro Phe Asp
115 120 125

Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Val Arg His Asp
130 135 140

Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu Tyr Ala Met Pro
145 150 155 160

Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys
165 170 175

Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met Leu Arg Leu
180 185 190

Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu Glu Glu Trp Ser
195 200 205

Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Thr Leu
210 215 220

Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser
225 230 235 240

Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala Phe Val Leu Ala
245 250 255

Asn Ile Leu Arg Gln Asn His Ser Lys Asn Met Leu Thr Ser Ser Ser
260 265 270

Thr Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu Trp Pro Gln Glu
275 280 285

Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu Ala Leu Ile Leu
290 295 300

Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg Ala Phe Phe Arg
305 310 315 320

Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Ser Leu Ser Xaa
325 330 335

Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro Asn
340 345 350

Asp Met Arg Arg Gly Leu Ile Arg His Leu Leu Ser Asp Pro Thr Gly
355 360 365

Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
370 375

<210> 49
<211> 524
<212> PRT
<213> Arabidopsis thaliana

<400> 49

Met Glu Cys Val Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr
1 5 10 15

Phe Pro Ser Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr
20 25 30

Ser Tyr Arg Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly
35 40 45

Gly Gly Ser Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe
50 55 60

Ala Asp Glu Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe
65 70 75 80

Val Gln Met Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val
85 90 95

Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val
100 105 110

Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala
115 120 125

Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
130 135 140

Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
145 150 155 160

Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp
165 170 175

Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg
180 185 190

Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
195 200 205

Tyr Leu Ser Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu
210 215 220

Arg Leu Val Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala
225 230 235 240

Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val
245 250 255

Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu
260 265 270

Val Glu Asn Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr
275 280 285

Arg Asp Tyr Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro
290 295 300

Thr Phe Leu Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu
305 310 315 320

Glu Thr Cys Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys

325 330 335

Thr Lys Leu Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys
340 345 350

Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro
355 360 365

Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val
370 375 380

His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro
385 390 395 400

Lys Tyr Ala Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys
405 410 415

Gln Ile Asn Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro
420 425 430

Pro Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu
435 440 445

Ile Val Gln Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe
450 455 460

Phe Arg Leu Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu
465 470 475 480

Thr Ser Gly Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser
485 490 495

Pro Asn Asn Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro
500 505 510

Thr Gly Ala Thr Met Ile Lys Thr Tyr Leu Lys Val
515 520

<210> 50
<211> 529
<212> PRT
<213> Adonis palaestina

<400> 50
Met Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp
1 5 10 15

Thr Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile
20 25 30

His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp
35 40 45

Gly Gly Ser Gly Ser Arg Ser Ser Val Ala Tyr Lys Glu Gly Phe Val
50 55 60

Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val
65 70 75 80

Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp

85 90 95

Lys Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val
100 105 110

Ile Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys
115 120 125

Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn
130 135 140

Asn Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg
145 150 155 160

Cys Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp
165 170 175

Ala Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu
180 185 190

Leu His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr
195 200 205

Leu Asp Ser Lys Val Glu Arg Ile Thr Glu Ala Gly Asp Gly His Ser
210 215 220

Leu Val Val Cys Glu Asn Glu Ile Phe Ile Pro Cys Arg Leu Ala Thr
225 230 235 240

Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly
245 250 255

Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val
260 265 270

Glu Asn Asn Pro Tyr Asp Pro Asn Leu Met Val Phe Met Asp Tyr Arg
275 280 285

Asp Tyr Met Gln Gln Lys Leu Gln Cys Ser Glu Glu Glu Tyr Pro Thr
290 295 300

Phe Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu
305 310 315 320

Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg
325 330 335

Lys Leu Met Ser Arg Leu Lys Thr Leu Gly Ile Gln Val Thr Lys Val
340 345 350

Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
355 360 365

Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
370 375 380

Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys
385 390 395 400

Tyr Ala Ser Val Ile Ala Lys Ile Leu Lys Gln Asp Asn Ser Ala Tyr
405 410 415

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Val Val Ser Gly Gln Ser Ser Ala Val Asn Ile Ser Met Gln Ala Trp
            420                 425                 430

Ser Ser Leu Trp Pro Lys Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
        435                 440                 445

Phe Gly Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr
    450                 455                 460

Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe
465                 470                 475                 480

Leu Gly Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr
                485                 490                 495

Met Phe Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His
            500                 505                 510

Leu Leu Ser Asp Pro Ser Gly Ala Val Met Val Arg Ala Tyr Leu Glu
        515                 520                 525

Arg



<210> 51
<211> 529
<212> PRT
<213> Adonis palaestina

<400> 51
Met Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp
  1               5                  10                  15

Thr Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile
            20                  25                  30

His Arg Tyr Gly Ser Ser Cys Arg Val Asp Phe Gln Val Arg Ala Asp
        35                  40                  45

Gly Gly Ser Gly Ser Arg Thr Ser Val Ala Tyr Lys Glu Gly Phe Val
    50                  55                  60

Asp Glu Glu Asp Phe Ile Lys Ala Gly Gly Ser Glu Leu Leu Phe Val
 65                  70                  75                  80

Gln Met Gln Gln Thr Lys Ser Met Glu Lys Gln Ala Lys Leu Ala Asp
                85                  90                  95

Lys Leu Pro Pro Ile Pro Phe Gly Glu Ser Val Met Asp Leu Val Val
            100                 105                 110

Ile Gly Cys Gly Pro Ala Gly Leu Ser Leu Ala Ala Glu Ala Ala Lys
        115                 120                 125

Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn
    130                 135                 140

Asn Tyr Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Glu Arg
145                 150                 155                 160
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Cys Ile Glu His Ala Trp Lys Asp Thr Ile Val Tyr Leu Asp Asn Asp
165 170 175

Ala Pro Val Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu
180 185 190

Leu His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr
195 200 205

Leu Asn Ser Lys Val Glu Arg Ile Thr Glu Ala Gly Asp Gly His Ser
210 215 220

Leu Val Val Cys Glu Asn Asp Ile Phe Ile Pro Cys Arg Leu Ala Thr
225 230 235 240

Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly
245 250 255

Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val
260 265 270

Glu Asn Asn Pro Tyr Asp Pro Asn Leu Met Val Phe Met Asp Tyr Arg
275 280 285

Asp Tyr Met Gln Gln Lys Leu Gln Cys Ser Glu Glu Glu Tyr Pro Thr
290 295 300

Phe Leu Tyr Val Met Pro Met Ser Pro Thr Arg Leu Phe Phe Glu Glu
305 310 315 320

Thr Cys Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Arg
325 330 335

Lys Leu Met Ser Arg Leu Lys Thr Leu Gly Ile Gln Val Thr Lys Ile
340 345 350

Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn
355 360 365

Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His
370 375 380

Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys
385 390 395 400

Tyr Ala Ser Val Ile Ala Lys Ile Leu Lys Gln Asp Asn Ser Ala Tyr
405 410 415

Val Val Ser Gly Gln Ser Ser Ala Val Asn Ile Ser Met Gln Ala Trp
420 425 430

Ser Ser Leu Trp Pro Lys Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu
435 440 445

Phe Gly Leu Glu Leu Ile Val Gln Leu Asp Ile Glu Ala Thr Arg Thr
450 455 460

Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp Trp Gly Phe
465 470 475 480

Leu Gly Ser Ser Leu Ser Ser Phe Asp Leu Val Leu Phe Ser Met Tyr

485 490 495

Met Phe Val Leu Ala Pro Asn Ser Met Arg Met Ser Leu Val Arg His
500 505 510

Leu Leu Ser Asp Pro Ser Gly Ala Val Met Val Lys Ala Tyr Leu Glu
515 520 525

Arg

<210> 52
<211> 533
<212> PRT
<213> Lettuce

<400> 52
Met Glu Cys Phe Gly Ala Arg Asn Met Thr Ala Thr Met Ala Val Phe
1 5 10 15

Thr Cys Pro Arg Phe Thr Asp Cys Asn Ile Arg His Lys Phe Ser Leu
20 25 30

Leu Lys Gln Arg Arg Phe Thr Asn Leu Ser Ala Ser Ser Ser Leu Arg
35 40 45

Gln Ile Lys Cys Ser Ala Lys Ser Asp Arg Cys Val Val Asp Lys Gln
50 55 60

Gly Ile Ser Val Ala Asp Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser
65 70 75 80

Glu Leu Phe Phe Val Gln Met Gln Arg Thr Lys Ser Met Glu Ser Gln
85 90 95

Ser Lys Leu Ser Glu Lys Leu Ala Gln Ile Pro Ile Gly Asn Cys Ile
100 105 110

Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala
115 120 125

Ala Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu Ile Gly Pro Asp
130 135 140

Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Gln Asp Glu Phe Ile Gly
145 150 155 160

Leu Gly Leu Glu Gly Cys Ile Glu His Ser Trp Lys Asp Thr Leu Val
165 170 175

Tyr Leu Asp Asp Ala Asp Pro Ile Arg Ile Gly Arg Ala Tyr Gly Arg
180 185 190

Val His Arg Asp Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu
195 200 205

Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala
210 215 220

Pro Asn Gly Tyr Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro

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225                     230                     235                     240

Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Phe Leu
                245                 250                 255

Glu Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly
            260                 265                 270

Ile Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro Asp Leu Met Val
        275                 280                 285

Phe Met Asp Tyr Arg Asp Phe Ser Lys His Lys Pro Glu Ser Leu Glu
    290                 295                 300

Ala Lys Tyr Pro Thr Phe Leu Tyr Val Met Ala Met Ser Pro Thr Lys
305                 310                 315                 320

Ile Phe Phe Glu Glu Thr Cys Leu Ala Ser Arg Glu Ala Met Pro Phe
                325                 330                 335

Asn Leu Leu Lys Ser Lys Leu Met Ser Arg Leu Lys Ala Met Gly Ile
            340                 345                 350

Arg Ile Thr Arg Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly
        355                 360                 365

Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala
    370                 375                 380

Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu
385                 390                 395                 400

Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Arg Gln
                405                 410                 415

Asp Gln Ser Lys Glu Met Ile Ser Leu Gly Lys Tyr Thr Asn Ile Ser
            420                 425                 430

Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg
        435                 440                 445

Ala Phe Phe Leu Phe Gly Leu Ser His Ile Val Leu Met Asp Leu Glu
    450                 455                 460

Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Lys Trp Met
465                 470                 475                 480

Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile
                485                 490                 495

Phe Ala Leu Tyr Met Phe Val Ile Ala Pro His Ser Leu Arg Met Glu
            500                 505                 510

Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Ala Thr Met Val Lys
        515                 520                 525

Ala Tyr Leu Thr Ile
    530
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<210> 53

<211> 526
<212> PRT
<213> Tomato

<400> 53
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Met Glu Cys Val Gly Val Gln Asn Val Gly Ala Met Ala Val Leu Thr
 1               5                  10                  15

Arg Pro Arg Leu Asn Arg Trp Ser Gly Gly Glu Leu Cys Gln Glu Lys
            20                  25                  30

Ser Ile Phe Leu Ala Tyr Glu Gln Tyr Glu Ser Lys Cys Asn Ser Ser
        35                  40                  45

Ser Gly Ser Asp Ser Cys Val Val Asp Lys Glu Asp Phe Ala Asp Glu
    50                  55                  60

Glu Asp Tyr Ile Lys Ala Gly Gly Ser Gln Leu Val Phe Val Gln Met
65                  70                  75                  80

Gln Gln Lys Lys Asp Met Asp Gln Gln Ser Lys Leu Ser Asp Glu Leu
                85                  90                  95

Arg Gln Ile Ser Ala Gly Gln Thr Val Leu Asp Leu Val Val Ile Gly
            100                 105                 110

Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly
        115                 120                 125

Leu Asn Val Gly Leu Val Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr
    130                 135                 140

Gly Val Trp Glu Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile
145                 150                 155                 160

Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Glu Pro
                165                 170                 175

Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Phe Leu His
            180                 185                 190

Glu Glu Leu Leu Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn
        195                 200                 205

Ser Lys Val Asp Arg Ile Val Glu Ala Thr Asn Gly Gln Ser Leu Val
    210                 215                 220

Glu Cys Glu Gly Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala
225                 230                 235                 240

Ser Gly Ala Ala Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Ser Pro
                245                 250                 255

Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn
            260                 265                 270

Asn Pro Phe Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr
        275                 280                 285

Leu Arg His Asp Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu
    290                 295                 300
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Tyr Ala Met Pro Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys
305 310 315 320

Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu
325 330 335

Met Leu Arg Leu Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu
340 345 350

Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu
355 360 365

Gln Lys Thr Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala
370 375 380

Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala
385 390 395 400

Ser Val Leu Ala Asn Ile Leu Arg Gln His Tyr Ser Lys Asn Met Leu
405 410 415

Thr Ser Ser Ser Ile Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu
420 425 430

Trp Pro Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu
435 440 445

Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg
450 455 460

Ala Phe Phe Arg Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser
465 470 475 480

Ser Leu Ser Ser Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile
485 490 495

Ile Ala Pro Asn Asp Met Arg Lys Gly Leu Ile Arg His Leu Leu Ser
500 505 510

Asp Pro Thr Gly Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
515 520 525

<210> 54
<211> 516
<212> PRT
<213> Tagetes erecta

<400> 54
Met Ser Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr
1 5 10 15

Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys
20 25 30

Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu
35 40 45

Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
50 55 60

Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
65 70 75 80

Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
85 90 95

Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
100 105 110

Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
115 120 125

Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
130 135 140

Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu
145 150 155 160

Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser
165 170 175

Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly
180 185 190

Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn
195 200 205

Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg
210 215 220

Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr
225 230 235 240

Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu
245 250 255

Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met
260 265 270

Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln
275 280 285

Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe
290 295 300

Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu
305 310 315 320

Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile
325 330 335

Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser
340 345 350

Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser
355 360 365

Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu
370 375 380

Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn

385 390 395 400

Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys
405 410 415

Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala
420 425 430

Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
435 440 445

Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
450 455 460

Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
465 470 475 480

Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
485 490 495

Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala
500 505 510

Tyr Leu Thr Ile
515

<210> 55
<211> 501
<212> PRT
<213> Arabidopsis thaliana

<400> 55
Met Asp Thr Leu Leu Lys Thr Pro Asn Lys Leu Asp Phe Phe Ile Pro
1 5 10 15

Gln Phe His Gly Phe Glu Arg Leu Cys Ser Asn Asn Pro Tyr His Ser
20 25 30

Arg Val Arg Leu Gly Val Lys Lys Arg Ala Ile Lys Ile Val Ser Ser
35 40 45

Val Val Ser Gly Ser Ala Ala Leu Leu Asp Leu Val Pro Glu Thr Lys
50 55 60

Lys Glu Asn Leu Asp Phe Glu Leu Pro Leu Tyr Asp Thr Ser Lys Ser
65 70 75 80

Gln Val Val Asp Leu Ala Ile Val Gly Gly Gly Pro Ala Gly Leu Ala
85 90 95

Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile Asp
100 105 110

Pro Ser Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val Asp
115 120 125

Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr Thr Trp Ser
130 135 140

Gly Ala Val Val Tyr Val Asp Glu Gly Val Lys Lys Asp Leu Ser Arg

145 150 155 160

Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Leu Gln
165 170 175

Lys Cys Ile Thr Asn Gly Val Lys Phe His Gln Ser Lys Val Thr Asn
180 185 190

Val Val His Glu Glu Ala Asn Ser Thr Val Val Cys Ser Asp Gly Val
195 200 205

Lys Ile Gln Ala Ser Val Val Leu Asp Ala Thr Gly Phe Ser Arg Cys
210 215 220

Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala Tyr
225 230 235 240

Gly Ile Val Ala Glu Val Asp Gly His Pro Phe Asp Val Asp Lys Met
245 250 255

Val Phe Met Asp Trp Arg Asp Lys His Leu Asp Ser Tyr Pro Glu Leu
260 265 270

Lys Glu Arg Asn Ser Lys Ile Pro Thr Phe Leu Tyr Ala Met Pro Phe
275 280 285

Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg Pro
290 295 300

Gly Leu Arg Met Glu Asp Ile Gln Glu Arg Met Ala Ala Arg Leu Lys
305 310 315 320

His Leu Gly Ile Asn Val Lys Arg Ile Glu Glu Asp Glu Arg Cys Val
325 330 335

Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val Gly
340 345 350

Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met Val
355 360 365

Ala Arg Thr Leu Ala Ala Ala Pro Ile Val Ala Asn Ala Ile Val Arg
370 375 380

Tyr Leu Gly Ser Pro Ser Ser Asn Ser Leu Arg Gly Asp Gln Leu Ser
385 390 395 400

Ala Glu Val Trp Arg Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg
405 410 415

Glu Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Asp
420 425 430

Ala Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Gln Pro His Tyr
435 440 445

Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu Val
450 455 460

Phe Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Leu Glu
465 470 475 480

Ile Met Thr Lys Gly Thr Val Pro Leu Ala Lys Met Ile Asn Asn Leu
485 490 495

Val Gln Asp Arg Asp
500

<210> 56
<211> 502
<212> PRT
<213> Adonis palaestina

<400> 56
Met Asp Thr Leu Leu Arg Thr His Asn Lys Leu Glu Leu Leu Pro Thr
1 5 10 15

Leu His Gly Phe Ala Glu Lys Gln His Leu Val Ser Thr Ser Lys Leu
20 25 30

Gln Asn Gln Val Phe Arg Ile Ala Ser Arg Asn Ile His Pro Cys Arg
35 40 45

Asn Gly Thr Val Lys Ala Arg Gly Ser Ala Leu Leu Glu Leu Val Pro
50 55 60

Glu Thr Lys Lys Glu Asn Leu Glu Phe Asp Leu Pro Ala Tyr Asp Pro
65 70 75 80

Ser Arg Gly Ile Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala
85 90 95

Gly Leu Ala Ile Ala Gln Gln Val Ser Glu Ala Gly Leu Leu Val Cys
100 105 110

Ser Ile Asp Pro Ser Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val
115 120 125

Trp Val Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr
130 135 140

Thr Trp Ser Gly Ala Val Val Tyr Thr Asp Asp Asn Ser Lys Lys Tyr
145 150 155 160

Leu Asp Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys
165 170 175

Met Leu Gln Lys Cys Val Thr Asn Gly Val Lys Phe His Gln Ala Lys
180 185 190

Val Ile Lys Val Ile His Glu Glu Ser Lys Ser Leu Leu Ile Cys Asn
195 200 205

Asp Gly Ile Thr Ile Asn Ala Thr Val Val Leu Asp Ala Thr Gly Phe
210 215 220

Ser Arg Cys Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln
225 230 235 240

Val Ala Tyr Gly Ile Met Ala Glu Val Glu Glu His Pro Phe Asp Leu
245 250 255

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Asp Lys Met Leu Phe Met Asp Trp Arg Asp Ser His Leu Asn Glu Lys
            260                 265                 270

Leu Glu Leu Lys Asp Lys Asn Arg Lys Ile Pro Thr Phe Leu Tyr Ala
        275                 280                 285

Met Pro Phe Ser Ser Thr Lys Ile Phe Leu Glu Glu Thr Ser Leu Val
    290                 295                 300

Ala Arg Pro Gly Leu Arg Phe Glu Asp Ile Gln Glu Arg Met Val Ala
305                 310                 315                 320

Arg Leu Lys His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu
                325                 330                 335

Arg Cys Val Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg
            340                 345                 350

Val Val Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly
        355                 360                 365

Tyr Met Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Lys Ser
    370                 375                 380

Ile Val Gln Tyr Leu Gly Ser Asp Arg Ser Leu Ser Gly Asn Glu Leu
385                 390                 395                 400

Ser Ala Glu Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln
                405                 410                 415

Arg Glu Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu
            420                 425                 430

Gln Gly Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro His
        435                 440                 445

Tyr Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu
    450                 455                 460

Phe Phe Gly Leu Ser Leu Phe Ser His Ala Ser Asn Ala Ser Arg Ile
465                 470                 475                 480

Glu Ile Met Ala Lys Gly Thr Val Pro Leu Val Asn Met Met Asn Asn
                485                 490                 495

Leu Ile Gln Asp Thr Asp
            500


&lt;210&gt; 57
&lt;211&gt; 498
&lt;212&gt; PRT
&lt;213&gt; Pepper

&lt;400&gt; 57
Met Asp Thr Leu Leu Arg Thr Pro Asn Asn Leu Glu Phe Leu His Gly
  1               5                  10                  15

Phe Gly Val Lys Val Ser Ala Phe Ser Ser Val Lys Ser Gln Lys Phe
             20                  25                  30
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Gly Ala Lys Lys Phe Cys Glu Gly Leu Gly Ser Arg Ser Val Cys Val
35 40 45

Lys Ala Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr Lys Lys
50 55 60

Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys Gly Val
65 70 75 80

Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu Ala Val
85 90 95

Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile Asp Pro
100 105 110

Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
115 120 125

Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp Ser Gly
130 135 140

Ala Ala Val Tyr Ile Asp Asp Lys Thr Thr Lys Asp Leu Asn Arg Pro
145 150 155 160

Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met Gln Lys
165 170 175

Cys Ile Leu Asn Gly Val Lys Phe His Gln Ala Lys Val Ile Lys Val
180 185 190

Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly Ile Thr
195 200 205

Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg Ser Leu
210 215 220

Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala Tyr Gly
225 230 235 240

Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys Met Val
245 250 255

Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Val Glu Leu Lys
260 265 270

Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro Phe Ser
275 280 285

Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg Pro Gly
290 295 300

Leu Gly Met Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu Ser His
305 310 315 320

Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys Val Ile
325 330 335

Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val Gly Ile
340 345 350

Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met Val Ala

355 360 365

Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile Gln Tyr
370 375 380

Leu Ser Ser Glu Arg Ser His Ser Gly Asp Glu Leu Ser Ala Ala Val
385 390 395 400

Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu Phe Phe
405 410 415

Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala Thr Arg
420 425 430

Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp His Gly
435 440 445

Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe Gly Leu
450 455 460

Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Leu Glu Ile Met Thr
465 470 475 480

Lys Gly Thr Leu Pro Leu Val His Met Ile Asn Asn Leu Leu Gln Asp
485 490 495

Lys Glu

<210> 58
<211> 500
<212> PRT
<213> Tomato

<400> 58
Met Asp Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro
1 5 10 15

His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His
20 25 30

His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val
35 40 45

Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
50 55 60

Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
65 70 75 80

Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
85 90 95

Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile
100 105 110

Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val
115 120 125

Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp

130 135 140

Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His
145 150 155 160

Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met
165 170 175

Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile
180 185 190

Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly
195 200 205

Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg
210 215 220

Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala
225 230 235 240

Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys
245 250 255

Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp
260 265 270

Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro
275 280 285

Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg
290 295 300

Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu
305 310 315 320

Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys
325 330 335

Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val
340 345 350

Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met
355 360 365

Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile
370 375 380

Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr
385 390 395 400

Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
405 410 415

Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
420 425 430

Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
435 440 445

His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe
450 455 460

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Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
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Gln Asp Lys Glu
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His Lys Phe Gly Ser Arg Lys Ile Cys Glu Asn Trp Gly Lys Gly Val
         35                  40                  45

Cys Val Lys Ala Lys Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
     50                  55                  60

Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
 65                  70                  75                  80

Gly Leu Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
                 85                  90                  95

Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Val Ser Ile
            100                 105                 110

Asp Pro Ser Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val
        115                 120                 125

Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp
    130                 135                 140

Ser Gly Thr Val Val Tyr Ile Asp Asp Asn Thr Thr Lys Asp Leu Asp
145                 150                 155                 160

Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met
                165                 170                 175

Gln Lys Cys Ile Leu Asn Gly Val Lys Phe His His Ala Lys Val Ile
            180                 185                 190

Lys Val Ile His Glu Glu Ala Lys Ser Met Leu Ile Cys Asn Asp Gly
        195                 200                 205

Val Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg
    210                 215                 220

Cys Leu Val Gln Tyr Asp Lys Pro Tyr Lys Pro Gly Tyr Gln Val Ala
225                 230                 235                 240
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Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Thr Ser Lys
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Met Val Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Asn Met Glu
260 265 270

Leu Lys Glu Arg Asn Arg Lys Val Pro Thr Phe Leu Tyr Ala Met Pro
275 280 285

Phe Ser Ser Asn Lys Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg
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Pro Gly Leu Arg Met Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu
305 310 315 320

Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys
325 330 335

Val Ile Pro Met Gly Gly Ser Leu Pro Val Ile Pro Gln Arg Val Val
340 345 350

Gly Thr Gly Gly Thr Ala Gly Leu Val His Pro Ser Thr Gly Tyr Met
355 360 365

Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile
370 375 380

His Tyr Leu Gly Ser Glu Lys Asp Leu Leu Gly Asn Glu Leu Ser Ala
385 390 395 400

Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
405 410 415

Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
420 425 430

Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
435 440 445

His Gly Phe Leu Ser Ser Arg Leu Tyr Leu Pro Glu Leu Ile Phe Phe
450 455 460

Gly Leu Ser Leu Phe Ser Arg Ala Ser Asn Thr Ser Arg Ile Glu Ile
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Met Thr Lys Gly Thr Leu Pro Leu Val Asn Met Ile Asn Asn Leu Leu
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Gln Asp Thr Glu
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            20                  25                  30

Ser Lys Ser Gln Phe Gln Asp Phe Arg Phe Gly Pro Lys Lys Ser Gln
        35                  40                  45

Phe Lys Leu Gly Gln Lys Tyr Cys Val Lys Ala Ser Ser Ser Ala Leu
    50                  55                  60

Leu Glu Leu Val Pro Glu Ile Lys Lys Glu Asn Leu Asp Phe Asp Leu
65                  70                  75                  80

Pro Met Tyr Asp Pro Ser Arg Asn Val Val Val Asp Leu Val Val Val
                85                  90                  95

Gly Gly Gly Pro Ser Gly Leu Ala Val Ala Gln Gln Val Ser Glu Ala
            100                 105                 110

Gly Leu Thr Val Cys Ser Ile Asp Pro Ser Pro Lys Leu Ile Trp Pro
        115                 120                 125

Asn Asn Tyr Gly Val Trp Val Asp Glu Phe Glu Ala Met Asp Leu Leu
    130                 135                 140

Asp Cys Leu Asp Thr Thr Trp Ser Ser Ala Val Val Tyr Ile Asp Glu
145                 150                 155                 160

Lys Ser Thr Lys Ser Leu Asn Arg Pro Tyr Ala Arg Val Asn Arg Lys
                165                 170                 175

Gln Leu Lys Thr Lys Met Leu Gln Lys Cys Ile Ala Asn Gly Val Lys
            180                 185                 190

Phe His Gln Ala Lys Val Ile Lys Val Ile His Glu Glu Leu Lys Ser
        195                 200                 205

Leu Leu Ile Cys Asn Asp Gly Val Thr Ile Gln Ala Thr Leu Val Leu
    210                 215                 220

Asp Ala Thr Gly Phe Ser Arg Ser Leu Val Gln Tyr Asp Lys Pro Tyr
225                 230                 235                 240

Asn Pro Gly Tyr Gln Val Ala Tyr Gly Ile Leu Ala Glu Val Glu Glu
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His Pro Phe Asp Val Asp Lys Met Leu Phe Met Asp Trp Arg Asp Ser
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Thr Phe Leu Tyr Ala Met Pro Phe Ser Ser Thr Arg Ile Phe Leu Glu
    290                 295                 300

Glu Thr Ser Leu Val Ala Arg Pro Gly Leu Lys Met Glu Asp Ile Gln
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Glu Arg Met Ala Tyr Arg Leu Lys His Leu Gly Ile Lys Val Lys Ser
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Ile Glu Glu Asp Glu Arg Cys Val Ile Pro Met Gly Gly Pro Leu Pro
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            340                 345                 350

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His Pro Ser Thr Gly Tyr Met Val Ala Arg Thr Leu Ala Ala Ala Pro
    370                 375                 380

Ile Val Ala Lys Ser Ile Ile Arg Tyr Leu Asn Asn Glu Lys Ser Met
385                 390                 395                 400

Val Ala Asp Val Thr Gly Asp Asp Leu Ala Ala Gly Ile Trp Arg Glu
                405                 410                 415

Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu Phe Phe Cys Phe Gly
            420                 425                 430

Met Asp Ile Leu Leu Lys Leu Asp Leu Glu Gly Thr Arg Arg Phe Phe
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Ser Arg Leu Phe Leu Pro Glu Leu Val Thr Phe Gly Leu Ser Leu Phe
465                 470                 475                 480

Gly His Ala Ser Asn Thr Cys Arg Val Glu Ile Met Ala Lys Gly Thr
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Leu Pro Leu Ala Thr Met Ile Gly Asn Leu Val Arg Asp Arg Glu
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Leu His Glu Leu Ala Lys Arg His Phe Leu Ser Pro Ser Pro Asn Pro
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Gln Asn Pro Asn Phe Lys Phe Phe Ser Arg Lys Pro Tyr Gln Lys Lys
         35                  40                  45

Cys Arg Asn Gly Tyr Ile Gly Val Ser Ser Asn Gln Leu Leu Asp Leu
     50                  55                  60

Val Pro Glu Ile Lys Lys Glu His Leu Glu Phe Asp Leu Pro Leu Tyr
 65                  70                  75                  80

Asp Pro Ser Lys Ala Leu Thr Leu Asp Leu Ala Val Val Gly Gly Gly
                 85                  90                  95

Pro Leu Ala Arg Ser Cys Ser Thr Ser Leu Gly Gly Gly Leu Ser Val
            100                 105                 110

Val Ser Ile Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly
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115 120 125

Val Trp Val Asp Glu Phe Glu Asp Met Asp Leu Leu Asp Cys Leu Asp
130 135 140

Ala Thr Trp Ser Gly Ala Ile Val Tyr Val Asp Asp Arg Ser Thr Lys
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Asn Leu Ser Arg Pro Tyr Ala Arg Val Asn Arg Lys Asn Leu Lys Ser
165 170 175

Lys Met Met Lys Lys Cys Val Ser Asn Gly Val Arg Phe His Gln Ala
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Thr Val Val Lys Ala Met His Glu Glu Glu Lys Ser Tyr Leu Ile Cys
195 200 205

Ser Asp Gly Val Thr Ile Asp Ala Arg Val Val Leu Asp Ala Thr Gly
210 215 220

Phe Ser Arg Cys Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr
225 230 235 240

Gln Val Ala Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp
245 250 255

Val Asp Lys Met Val Phe Met Asp Trp Arg Asp Ser His Leu Asn Gly
260 265 270

Lys Ala Glu Leu Asn Glu Arg Asn Ala Lys Ile Pro Thr Phe Leu Tyr
275 280 285

Ala Met Pro Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu
290 295 300

Val Ala Arg Pro Gly Leu Lys Met Glu Asp Ile Gln Glu Arg Met Val
305 310 315 320

Ala Arg Leu Asn His Leu Gly Ile Arg Ile Lys Ser Ile Glu Glu Asp
325 330 335

Glu Arg Cys Val Ile Pro Met Gly Gly Pro Leu Pro Val Ile Pro Gln
340 345 350

Arg Val Val Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr
355 360 365

Gly Tyr Met Val Ala Arg Thr Leu Ala Ala Ala Pro Ile Val Ala Asn
370 375 380

Ser Ile Val Gln Tyr Leu Val Ser Asp Ser Gly Leu Ser Gly Asn Asp
385 390 395 400

Leu Ser Ala Asp Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg
405 410 415

Gln Arg Glu Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp
420 425 430

Leu Glu Gly Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro
435 440 445

Arg Tyr Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu
    450   455   460

Val Pro Phe Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Cys Lys
465   470   475   480

Leu Glu Ile Met Ala Lys Gly Thr Leu Pro Leu Val Asn Met Ile Asn
                485   490   495

Asn Leu Val Gln Asp Arg Asp
            500

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/12121

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.
US CL :435/189, 193, 233, 252.3, 320.1, 325; 536/23.2
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/189, 193, 233, 252.3, 320.1, 325; 536/23.2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97/36998 A1 (UNIVERSITY OF MARYLAND COLLEGE PARK) 09 October 1997, see entire document, especially SEQ ID No:1.	1-8

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
02 AUGUST 1999	15 SEP 1999

Name and mailing address of the ISA/US	Authorized officer
Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	D. Lawrence for BRADLEY S. MAYHEW
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/12121

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

C12N 1/21, 5/10, 9/10, 15/53, 15/54, 15/61, 15/63; C12P 23/00; C12Q 1/68

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

Dialog and APS
search terms: IPP, epsilon cyclase, lycopene cyclase, isopentenyl pyrophosphate isomerase and isopentenyl diphosphate isomerase